

TABLE 1: GENES IN THE APPLICATION

HMP:

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 1 | 2 | RXS02735 | VW0074 | 14576 | 15280 | 6-Phosphoglucolactonase |
| 3 | 4 | RXA01626 | GR00452 | 4270 | 3926 | L-ribulose-phosphate 4-epimerase |
| 5 | 6 | RXA02245 | GR00654 | 13639 | 14295 | RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1) |
| 7 | 8 | RXA01015 | GR00290 | 346 | 5 | RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6) |

TCA:

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 9 | 10 | RXN01312 | VW0082 | 20803 | 18785 | SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1) |
| 11 | 12 | F RXA01312 | GR00380 | 2690 | 1614 | SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1) |
| 13 | 14 | RXN00231 | VW0083 | 15484 | 14015 | SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16) |
| 15 | 16 | RXA01311 | GR00380 | 1611 | 865 | SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1) |
| 17 | 18 | RXA01535 | GR00427 | 1354 | 2760 | FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2) |
| 19 | 20 | RXA00517 | GR00131 | 1407 | 2447 | MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82) |
| 21 | 22 | RXA01350 | GR00392 | 1844 | 2827 | MALATE DEHYDROGENASE (EC 1.1.1.37) |

EMB-Pathway

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 23 | 24 | RXA02149 | GR00639 | 17786 | 18754 | GLUCOKINASE (EC 2.7.1.2) |
| 25 | 26 | RXA01814 | GR00515 | 2571 | 910 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 27 | 28 | RXN02803 | VW0086 | 1 | 657 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 29 | 30 | F RXA02803 | GR00784 | 2 | 400 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 31 | 32 | RXN03076 | VW0043 | 1624 | 35 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 33 | 34 | F RXA02854 | GR10002 | 1588 | 5 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 35 | 36 | RXA00511 | GR00129 | 1 | 513 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |

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|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 37 | 38 | RXN01365 | VV0091 | 1476 | 103 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 39 | 40 | F RXA01365 | GR00397 | 897 | 4 | PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8) |
| 41 | 42 | RXA00098 | GR00014 | 6525 | 8144 | GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) |
| 43 | 44 | RXA01989 | GR00578 | 1 | 630 | GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9) |
| 45 | 46 | RXA00340 | GR00059 | 1549 | 2694 | PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) |
| 47 | 48 | RXA02492 | GR00720 | 2201 | 2917 | PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) |
| 49 | 50 | RXA00381 | GR00082 | 1451 | 846 | PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) |
| 51 | 52 | RXA02122 | GR00636 | 6511 | 5813 | PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) |
| 53 | 54 | RXA00206 | GR00032 | 6171 | 5134 | 6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11) |
| 55 | 56 | RXA01243 | GR00359 | 2302 | 3261 | 1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56) |
| 57 | 58 | RXA01882 | GR00538 | 1165 | 2154 | 1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56) |
| 59 | 60 | RXA01702 | GR00479 | 1397 | 366 | FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13) |
| 61 | 62 | RXA02258 | GR00654 | 26451 | 27227 | TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) |
| 63 | 64 | RXN01225 | VV0064 | 6382 | 4943 | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) |
| 65 | 66 | F RXA01225 | GR00354 | 5302 | 6741 | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE HOMOLOG |
| 67 | 68 | RXA02256 | GR00654 | 23934 | 24935 | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) |
| 69 | 70 | RXA02257 | GR00654 | 25155 | 26369 | PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) |
| 71 | 72 | RXA00235 | GR00036 | 2365 | 1091 | ENOLASE (EC 4.2.1.11) |
| 73 | 74 | RXA01093 | GR00306 | 1552 | 122 | PYRUVATE KINASE (EC 2.7.1.40) |
| 75 | 76 | RXN02675 | VV0098 | 72801 | 70945 | PYRUVATE KINASE (EC 2.7.1.40) |
| 77 | 78 | F RXA02675 | GR00754 | 2 | 364 | PYRUVATE KINASE (EC 2.7.1.40) |
| 79 | 80 | F RXA02695 | GR00755 | 2949 | 4370 | PYRUVATE KINASE (EC 2.7.1.40) |
| 81 | 82 | RXA00682 | GR00179 | 5299 | 3401 | PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2) |
| 83 | 84 | RXA00683 | GR00179 | 6440 | 5349 | PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2) |
| 85 | 86 | RXN00635 | VV0135 | 22708 | 20972 | PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2) |
| 87 | 88 | F RXA02807 | GR00788 | 88 | 552 | PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2) |
| 89 | 90 | F RXA00635 | GR00167 | 3 | 923 | PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2.2) |
| 91 | 92 | RXN03044 | VV0019 | 1391 | 2221 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 93 | 94 | F RXA02852 | GR00852 | 3 | 281 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 95 | 96 | F RXA00268 | GR00041 | 125 | 955 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 97 | 98 | RXN03086 | VV0049 | 2243 | 2650 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 99 | 100 | F RXA02887 | GR10022 | 411 | 4 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 101 | 102 | RXN03043 | VV0019 | 1 | 1362 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 103 | 104 | F RXA02897 | GR10039 | 1291 | 5 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 105 | 106 | RXN03083 | VV0047 | 88 | 1110 | DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) |
| 107 | 108 | F RXA02853 | GR10001 | 89 | 1495 | DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) |
| 109 | 110 | RXA02259 | GR00654 | 27401 | 30172 | PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31) |
| 111 | 112 | RXN02326 | VV0047 | 4500 | 5315 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 113 | 114 | F RXA02326 | GR00668 | 5338 | 4523 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 115 | 116 | RXN02327 | VV0047 | 3533 | 4492 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 117 | 118 | F RXA02327 | GR00668 | 6305 | 5346 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 119 | 120 | RXN02328 | VV0047 | 1842 | 3437 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 121 | 122 | F RXA02328 | GR00668 | 7783 | 6401 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 123 | 124 | RXN01048 | VV0079 | 12539 | 11316 | MALIC ENZYME (EC 1.1.1.39) |

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|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 125 | 126 | F RXA01048 | GR00296 | 3 | 290 | MALIC ENZYME (EC 1.1.1.39) |
| 127 | 128 | F RXA00290 | GR00046 | 4693 | 5655 | MALIC ENZYME (EC 1.1.1.39) |
| 129 | 130 | RXA02694 | GR00755 | 1879 | 2820 | L-LACTATE DEHYDROGENASE (EC 1.1.1.27) |
| 131 | 132 | RXN00296 | VV0176 | 35763 | 38606 | D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4) |
| 133 | 134 | F RXA00296 | GR00048 | 3 | 2837 | D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4) |
| 135 | 136 | RXA01901 | GR00544 | 4158 | 5417 | L-LACTATE DEHYDROGENASE (EC 1.1.2.3) |
| 137 | 138 | RXN01952 | VV0105 | 9954 | 11666 | D-LACTATE DEHYDROGENASE (EC 1.1.1.28) |
| 139 | 140 | F RXA01952 | GR00562 | 1 | 216 | D-LACTATE DEHYDROGENASE (EC 1.1.1.28) |
| 141 | 142 | F RXA01955 | GR00562 | 4611 | 6209 | D-LACTATE DEHYDROGENASE (EC 1.1.1.28) |
| 143 | 144 | RXA00293 | GR00047 | 2645 | 1734 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 145 | 146 | RXN01130 | VV0157 | 6138 | 5536 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 147 | 148 | F RXA01130 | GR00315 | 2 | 304 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 149 | 150 | RXN03112 | VV0085 | 509 | 6 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 151 | 152 | F RXA01133 | GR00316 | 568 | 1116 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 153 | 154 | RXN00871 | VV0127 | 3127 | 2240 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 155 | 156 | F RXA00871 | GR00239 | 2344 | 3207 | IOLB PROTEIN |
| | | | | | | IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE. |
| 157 | 158 | RXN02829 | VV0354 | 287 | 559 | IOLS PROTEIN |
| 159 | 160 | F RXA02829 | GR00816 | 287 | 562 | IOLS PROTEIN |
| 161 | 162 | RXN01468 | VV0019 | 7474 | 8298 | NAGD PROTEIN |
| 163 | 164 | F RXA01468 | GR00422 | 1250 | 2074 | PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE |
| 165 | 166 | RXA00794 | GR00211 | 3993 | 2989 | GLPX PROTEIN |
| 167 | 168 | RXN02920 | VV0213 | 6135 | 5224 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 169 | 170 | F RXA02379 | GR00690 | 1390 | 686 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) |
| 171 | 172 | RXN02688 | VV0098 | 59053 | 58385 | PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) |
| 173 | 174 | RXN03087 | VV0052 | 3216 | 3428 | PYRUVATE CARBOXYLASE (EC 6.4.1.1) |
| 175 | 176 | RXN03186 | VV0377 | 310 | 519 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 177 | 178 | RXN03187 | VV0382 | 3 | 281 | PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1) |
| 179 | 180 | RXN02591 | VV0098 | 14370 | 12541 | PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32) |
| 181 | 182 | RXS01260 | VV0009 | 3477 | 2296 | LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4) |
| | | | | | | LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED- CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4) |
| 183 | 184 | RXS01261 | VV0009 | 3703 | 3533 | GLYCEROL KINASE (EC 2.7.1.30) |

Glycerol metabolism

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 185 | 186 | RXA02640 | GR00749 | 1400 | 2926 | GLYCEROL KINASE (EC 2.7.1.30) |
| 187 | 188 | RXN01025 | VV0143 | 5483 | 4488 | GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P) ⁺) (EC 1.1.1.94) |
| 189 | 190 | F RXA01025 | GR00293 | 939 | 1853 | GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P) ⁺) (EC 1.1.1.94) |
| 191 | 192 | RXA01851 | GR00525 | 3515 | 1830 | AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5) |
| 193 | 194 | RXA01242 | GR00359 | 1526 | 2302 | GLYCEROL-3-PHOSPHATE REGULON REPRESSOR |
| 195 | 196 | RXA02288 | GR00661 | 992 | 147 | GLYCEROL-3-PHOSPHATE REGULON REPRESSOR |

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 197 | 198 | RXN01891 | VV0122 | 24949 | 24086 | GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR |
| 199 | 200 | F RXA01891 | GR00541 | 1736 | 918 | GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR |
| 201 | 202 | RXA02414 | GR00703 | 3808 | 3062 | Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid) |
| 203 | 204 | RXN01580 | VV0122 | 22091 | 22807 | Glycerophosphoryl diester phosphodiesterase |

Acetate metabolism

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 205 | 206 | RXA01436 | GR00418 | 2547 | 1357 | ACETATE KINASE (EC 2.7.2.1) |
| 207 | 208 | RXA00686 | GR00179 | 8744 | 7941 | ACETATE OPERON REPRESSOR |
| 209 | 210 | RXA00246 | GR00037 | 4425 | 3391 | ALCOHOL DEHYDROGENASE (EC 1.1.1.1) |
| 211 | 212 | RXA01571 | GR00438 | 1360 | 1959 | ALCOHOL DEHYDROGENASE (EC 1.1.1.1) |
| 213 | 214 | RXA01572 | GR00438 | 1928 | 2419 | ALCOHOL DEHYDROGENASE (EC 1.1.1.1) |
| 215 | 216 | RXA01758 | GR00498 | 3961 | 2945 | ALCOHOL DEHYDROGENASE (EC 1.1.1.1) |
| 217 | 218 | RXA02539 | GR00726 | 11676 | 10159 | ALDEHYDE DEHYDROGENASE (EC 1.1.1.1) |
| 219 | 220 | RXN03061 | VV0034 | 108 | 437 | ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) |
| 221 | 222 | RXN03150 | VV0155 | 10678 | 10055 | ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) |
| 223 | 224 | RXN01340 | VV0033 | 3 | 860 | ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) |
| 225 | 226 | RXN01498 | VV0008 | 1598 | 3160 | ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) |
| 227 | 228 | RXN02674 | VV0315 | 15614 | 14163 | ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) |
| 229 | 230 | RXN00868 | VV0127 | 2230 | 320 | ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) |
| 231 | 232 | RXN01143 | VV0077 | 9372 | 8254 | ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) |
| 233 | 234 | RXN01146 | VV0264 | 243 | 935 | ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) |
| 235 | 236 | RXN01144 | VV0077 | 8237 | 7722 | ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18) |

Butanediol, diacetyl and acetoin formation

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 237 | 238 | RXA02474 | GR00715 | 8082 | 7309 | (S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76) |
| 239 | 240 | RXA02453 | GR00710 | 6103 | 5351 | ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5) |
| 241 | 242 | RXS01758 | VV0112 | 27383 | 28399 | ALCOHOL DEHYDROGENASE (EC 1.1.1.1) |

HMP-Cycle

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 243 | 244 | RXA02737 | GR00763 | 3312 | 1771 | GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) |
| 245 | 246 | RXA02738 | GR00763 | 4499 | 3420 | TRANSALDOLASE (EC 2.2.1.2) |
| 247 | 248 | RXA02739 | GR00763 | 6769 | 4670 | TRANSKETOLASE (EC 2.2.1.1) |
| 249 | 250 | RXA00965 | GR00270 | 1232 | 510 | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44) |
| 251 | 252 | RXN00999 | VV0106 | 2817 | 1366 | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44) |
| 253 | 254 | F RXA00999 | GR00283 | 3012 | 4448 | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44) |

Nucleotide sugar conversion

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 255 | 256 | RXN02596 | VV0098 | 48784 | 47582 | UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9) |
| 257 | 258 | F RXA02596 | GR00742 | 1 | 489 | UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9) |
| 259 | 260 | F RXA02642 | GR00749 | 5383 | 5880 | UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9) |
| 261 | 262 | RXA02572 | GR00737 | 2 | 646 | UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22) |
| 263 | 264 | RXA02485 | GR00718 | 2345 | 3445 | UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158) |
| 265 | 266 | RXA01216 | GR00352 | 2302 | 1202 | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) |
| 267 | 268 | RXA01259 | GR00367 | 987 | 130 | UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9) |
| 269 | 270 | RXA02028 | GR00616 | 573 | 998 | UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9) |
| 271 | 272 | RXA01262 | GR00367 | 8351 | 7191 | GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132) |
| 273 | 274 | RXA01377 | GR00400 | 3935 | 5020 | MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) |
| 275 | 276 | RXA02063 | GR00626 | 3301 | 4527 | GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (EC 2.7.7.27) |
| 277 | 278 | RXN00014 | VV0048 | 8848 | 9627 | GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24) |
| 279 | 280 | F RXA00014 | GR00002 | 4448 | 5227 | GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24) |
| 281 | 282 | RXA01570 | GR00438 | 427 | 1281 | GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24) |
| 283 | 284 | RXA02666 | GR00753 | 7260 | 6493 | D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40) |
| 285 | 286 | RXA00825 | GR00222 | 222 | 1154 | DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46) |

Inositol and ribitol metabolism

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 287 | 288 | RXA01887 | GR00539 | 4219 | 3209 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 289 | 290 | RXN00013 | VV0048 | 7966 | 8838 | MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25) |
| 291 | 292 | F RXA00013 | GR00002 | 3566 | 4438 | MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1.3.25) |
| 293 | 294 | RXA01099 | GR00306 | 6328 | 5504 | INOSITOL MONOPHOSPHATE PHOSPHATASE |
| 295 | 296 | RXN01332 | VV0273 | 579 | 4 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 297 | 298 | F RXA01332 | GR00388 | 552 | 4 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 299 | 300 | RXA01632 | GR00454 | 2338 | 3342 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 301 | 302 | RXA01633 | GR00454 | 3380 | 4462 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 303 | 304 | RXN01406 | VV0278 | 2999 | 1977 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 305 | 306 | RXN01630 | VV0050 | 48113 | 47037 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 307 | 308 | RXN00528 | VV0079 | 23406 | 22318 | MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) |
| 309 | 310 | RXN03057 | VV0028 | 7017 | 7688 | MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18) |
| 311 | 312 | F RXA02902 | GR10040 | 10277 | 10948 | GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28) |
| 313 | 314 | RXA00251 | GR00038 | 931 | 224 | RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56) |

Utilization of sugars

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 315 | 316 | RXN02654 | VV0090 | 12206 | 13090 | GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47) |
| 317 | 318 | F RXA02654 | GR00752 | 7405 | 8289 | GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47) |
| 319 | 320 | RXN01049 | VV0079 | 9633 | 11114 | GLUCONOKINASE (EC 2.7.1.12) |
| 321 | 322 | F RXA01049 | GR00296 | 1502 | 492 | GLUCONOKINASE (EC 2.7.1.12) |
| 323 | 324 | F RXA01050 | GR00296 | 1972 | 1499 | GLUCONOKINASE (EC 2.7.1.12) |
| 325 | 326 | RXA00202 | GR00032 | 1216 | 275 | D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR |
| 327 | 328 | RXN00872 | VV0127 | 6557 | 5604 | FRUCTOKINASE (EC 2.7.1.4) |
| 329 | 330 | F RXA00872 | GR00240 | 565 | 1086 | FRUCTOKINASE (EC 2.7.1.4) |
| 331 | 332 | RXN00799 | VV0009 | 58477 | 56834 | PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37) |
| 333 | 334 | F RXA00799 | GR00214 | 1 | 1584 | PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37) |
| 335 | 336 | RXA00032 | GR00003 | 12028 | 10520 | MANNITOL 2-DEHYDROGENASE (EC 1.1.1.167) |
| 337 | 338 | RXA02528 | GR00725 | 6880 | 7854 | FRUCTOSE REPRESSOR |
| 339 | 340 | RXN00316 | VV0006 | 7035 | 8180 | Hypothetical Oxidoreductase (EC 1.1.1.-) |
| 341 | 342 | F RXA00309 | GR00053 | 316 | 5 | GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28) |
| 343 | 344 | RXN00310 | VV0006 | 6616 | 7050 | GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28) |
| 345 | 346 | F RXA00310 | GR00053 | 735 | 301 | GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28) |
| 347 | 348 | RXA00041 | GR00007 | 1246 | 5 | SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) |
| 349 | 350 | RXA02026 | GR00615 | 725 | 6 | SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) |
| 351 | 352 | RXA02061 | GR00626 | 1842 | 349 | SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) |
| 353 | 354 | RXN01369 | VV0124 | 595 | 1776 | MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) |

| Nucleic Acid | | Amino Acid | | Identification Code | Contig. | NT Start | NT Stop | Function |
|--------------|--|------------|--|---------------------|---------|----------|---------|--|
| SEQ ID NO | | SEQ ID NO | | | | | | |
| 355 | | 356 | | F RXA01369 | GR00398 | 3 | 503 | MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) |
| 357 | | 358 | | F RXA01373 | GR00399 | 595 | 1302 | MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) |
| 359 | | 360 | | RXA02611 | GR00743 | 1 | 1752 | 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) |
| 361 | | 362 | | RXA02612 | GR00743 | 1793 | 3985 | 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) |
| 363 | | 364 | | RXN01884 | VV0184 | 1 | 1890 | GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33) |
| 365 | | 366 | | F RXA01884 | GR00539 | 3 | 1475 | GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33) |
| 367 | | 368 | | RXA01111 | GR00306 | 16981 | 17427 | GLYCOGEN OPERON PROTEIN GLX (EC 3.2.1.-) |
| 369 | | 370 | | RXN01550 | VV0143 | 14749 | 16260 | GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1) |
| 371 | | 372 | | F RXA01550 | GR00431 | 3 | 1346 | GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1) |
| 373 | | 374 | | RXN02100 | VV0318 | 2 | 2326 | GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1) |
| 375 | | 376 | | F RXA02100 | GR00631 | 3 | 920 | GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1) |
| 377 | | 378 | | F RXA02113 | GR00633 | 2 | 1207 | GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1) |
| 379 | | 380 | | RXA02147 | GR00639 | 15516 | 16532 | ALPHA-AMYLASE (EC 3.2.1.1) |
| 381 | | 382 | | RXA01478 | GR00422 | 10517 | 12352 | GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3) |
| 383 | | 384 | | RXA01888 | GR00539 | 4366 | 4923 | GLUCOSE-RESISTANCE AMYLASE REGULATOR |
| 385 | | 386 | | RXN01927 | VV0127 | 50623 | 49244 | XYLOLASE KINASE (EC 2.7.1.17) |
| 387 | | 388 | | F RXA01927 | GR00555 | 3 | 1118 | XYLOLASE KINASE (EC 2.7.1.17) |
| 389 | | 390 | | RXA02729 | GR00762 | 747 | 4 | RIBOKINASE (EC 2.7.1.15) |
| 391 | | 392 | | RXA02797 | GR00778 | 1739 | 2641 | RIBOKINASE (EC 2.7.1.15) |
| 393 | | 394 | | RXA02730 | GR00762 | 1768 | 731 | RIBOSE OPERON REPRESSOR |
| 395 | | 396 | | RXA02551 | GR00729 | 2193 | 2552 | 6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86) |
| 397 | | 398 | | RXA01325 | GR00385 | 5676 | 5005 | DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4) |
| 399 | | 400 | | RXA00195 | GR00030 | 543 | 1103 | 1-deoxy-D-xylose 5-phosphate reductoisomerase (EC 1.1.1.-) |
| 401 | | 402 | | RXA00196 | GR00030 | 1094 | 1708 | 1-deoxy-D-xylose 5-phosphate reductoisomerase (EC 1.1.1.-) |
| 403 | | 404 | | RXN01562 | VV0191 | 1230 | 3137 | 1-DEOXYXYLOLULOSE-5-PHOSPHATE SYNTHASE |
| 405 | | 406 | | F RXA01562 | GR00436 | 2 | 1039 | 1-DEOXYXYLOLULOSE-5-PHOSPHATE SYNTHASE |
| 407 | | 408 | | F RXA01705 | GR00480 | 971 | 1573 | 1-DEOXYXYLOLULOSE-5-PHOSPHATE SYNTHASE |
| 409 | | 410 | | RXN00879 | VV0099 | 8763 | 6646 | 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) |
| 411 | | 412 | | F RXA00879 | GR00242 | 5927 | 3828 | 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25), amylomaltase |
| 413 | | 414 | | RXN00043 | VV0119 | 3244 | 2081 | N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) |
| 415 | | 416 | | F RXA00043 | GR00007 | 3244 | 2081 | N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) |
| 417 | | 418 | | RXN01752 | VV0127 | 35265 | 33805 | N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-) |
| 419 | | 420 | | F RXA01839 | GR00520 | 1157 | 510 | N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-) |
| 421 | | 422 | | RXA01859 | GR00529 | 1473 | 547 | N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-) |
| 423 | | 424 | | RXA00042 | GR00007 | 2037 | 1279 | GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) |
| 425 | | 426 | | RXA01482 | GR00422 | 17271 | 15397 | GLUCOSAMINE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) |
| 427 | | 428 | | RXN03179 | VV0336 | 2 | 667 | URONATE ISOMERASE (EC 5.3.1.12) |
| 429 | | 430 | | F RXA02872 | GR10013 | 675 | 4 | URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12) |
| 431 | | 432 | | RXN03180 | VV0337 | 672 | 163 | URONATE ISOMERASE (EC 5.3.1.12) |
| 433 | | 434 | | F RXA02873 | GR10014 | 672 | 163 | URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12) |
| 435 | | 436 | | RXA02292 | GR00662 | 1611 | 2285 | GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18) |
| 437 | | 438 | | RXA02666 | GR00753 | 7260 | 6493 | D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40) |
| 439 | | 440 | | RXA00202 | GR00032 | 1216 | 275 | D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR |
| 441 | | 442 | | RXA02440 | GR00709 | 5097 | 4258 | D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR |
| 443 | | 444 | | RXN01569 | VV0009 | 41086 | 42444 | dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) |

| <u>Nucleic Acid</u> SEQ ID NO | <u>Amino Acid</u> SEQ ID NO | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|----------------------------------|--------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 445 | 446 | F RXA01569 | GR00438 | 2 | 427 | DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) |
| 447 | 448 | F RXA02055 | GR00624 | 7122 | 8042 | DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) |
| 449 | 450 | RXA00825 | GR00222 | 222 | 1154 | DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46) |
| 451 | 452 | RXA02054 | GR00624 | 6103 | 7119 | DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46) |
| 453 | 454 | RXN00427 | VW0112 | 7004 | 6219 | DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---) |
| 455 | 456 | F RXA00427 | GR00098 | 1591 | 2022 | DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.---) |
| 457 | 458 | RXA00327 | GR00057 | 10263 | 9880 | PROTEIN ARAJ |
| 459 | 460 | RXA00328 | GR00057 | 11147 | 10656 | PROTEIN ARAJ |
| 461 | 462 | RXA00329 | GR00057 | 12390 | 11167 | PROTEIN ARAJ |
| 463 | 464 | RXN01554 | VW0135 | 28686 | 26545 | GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39) |
| 465 | 466 | RXN03015 | VW0063 | 289 | 8 | UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22) |
| 467 | 468 | RXN03056 | VW0028 | 6258 | 6935 | PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---) |
| 469 | 470 | RXN03030 | VW0009 | 57006 | 56443 | PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3.2.1.37) |
| 471 | 472 | RXN00401 | VW0025 | 12427 | 11489 | 5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41) |
| 473 | 474 | RXN02125 | VW0102 | 23242 | 22442 | ALDOSE REDUCTASE (EC 1.1.1.21) |
| 475 | 476 | RXN00200 | VW0181 | 1679 | 5116 | arabinosyl transferase subunit B (EC 2.4.2.-) |
| 477 | 478 | RXN01175 | VW0017 | 39688 | 38303 | PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15) |
| 479 | 480 | RXN01376 | VW0091 | 5610 | 4750 | PUTATIVE GLYCOSYL TRANSFERASE WBIF |
| 481 | 482 | RXN01631 | VW0050 | 47021 | 46143 | PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---) |
| 483 | 484 | RXN01593 | VW0229 | 13274 | 12408 | NAGD PROTEIN |
| 485 | 486 | RXN00337 | VW0197 | 20369 | 21418 | GALACTOKINASE (EC 2.7.1.6) |
| 487 | 488 | RXS00584 | VW0323 | 5516 | 6640 | PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15) |
| 489 | 490 | RXS02574 | | | | BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52) |
| 491 | 492 | RXS03215 | | | | GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28) |
| 493 | 494 | F RXA01915 | GR00549 | 1 | 1008 | GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28) |
| 495 | 496 | RXS03224 | | | | CYCLOMALTODEXTRINASE (EC 3.2.1.54) |
| 497 | 498 | F RXA00038 | | | | CYCLOMALTODEXTRINASE (EC 3.2.1.54) |
| 499 | 500 | RXC00233 | GR00006 | 1417 | 260 | protein involved in sugar metabolism |
| 501 | 502 | RXC00236 | | | | Membrane Lipoprotein involved in sugar metabolism |
| 503 | 504 | RXC00271 | | | | Exported Protein involved in ribose metabolism |
| 505 | 506 | RXC00338 | | | | protein involved in sugar metabolism |
| 507 | 508 | RXC00362 | | | | Membrane Spanning Protein involved in metabolism of diols |
| 509 | 510 | RXC00412 | | | | Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism |
| 511 | 512 | RXC00526 | | | | ABC Transporter ATP-Binding Protein involved in sugar metabolism |
| 513 | 514 | RXC01004 | | | | Membrane Spanning Protein involved in sugar metabolism |
| 515 | 516 | RXC01017 | | | | Cytosolic Protein involved in sugar metabolism |
| 517 | 518 | RXC01021 | | | | Cytosolic Kinase involved in metabolism of sugars and thiamin |
| 519 | 520 | RXC01212 | | | | ABC Transporter ATP-Binding Protein involved in sugar metabolism |
| 521 | 522 | RXC01306 | | | | Membrane Spanning Protein involved in sugar metabolism |
| 523 | 524 | RXC01366 | | | | Cytosolic Protein involved in sugar metabolism |
| 525 | 526 | RXC01372 | | | | Cytosolic Protein involved in sugar metabolism |
| 527 | 528 | RXC01659 | | | | protein involved in sugar metabolism |

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 529 | 530 | RXC01663 | | | | protein involved in sugar metabolism |
| 531 | 532 | RXC01693 | | | | protein involved in sugar metabolism |
| 533 | 534 | RXC01703 | | | | Cytosolic Protein involved in sugar metabolism |
| 535 | 536 | RXC02254 | | | | Membrane Associated Protein involved in sugar metabolism |
| 537 | 538 | RXC02255 | | | | Cytosolic Protein involved in sugar metabolism |
| 539 | 540 | RXC02435 | | | | protein involved in sugar metabolism |
| 541 | 542 | F RXA02435 | GR00709 | 825 | 268 | Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid) |
| 543 | 544 | RXC03216 | | | | protein involved in sugar metabolism |

TCA-cycle

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|---|
| 545 | 546 | RXA02175 | GR00641 | 10710 | 9418 | CITRATE SYNTHASE (EC 4.1.3.7) |
| 547 | 548 | RXA02621 | GR00746 | 2647 | 1829 | CITRATE LYASE BETA CHAIN (EC 4.1.3.6) |
| 549 | 550 | RXN00519 | VV0144 | 5585 | 3372 | ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42) |
| 551 | 552 | F RXA00521 | GR00133 | 2 | 1060 | ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42) |
| 553 | 554 | RXN02209 | VV0304 | 1 | 1671 | ACONITATE HYDRATASE (EC 4.2.1.3) |
| 555 | 556 | F RXA02209 | GR00648 | 3 | 1661 | ACONITATE HYDRATASE (EC 4.2.1.3) |
| 557 | 558 | RXN02213 | VV0305 | 1378 | 2151 | ACONITATE HYDRATASE (EC 4.2.1.3) |
| 559 | 560 | F RXA02213 | GR00649 | 1330 | 2046 | ACONITATE HYDRATASE (EC 4.2.1.3) |
| 561 | 562 | RXA02056 | GR00625 | 3 | 2870 | 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2) |
| 563 | 564 | RXA01745 | GR00495 | 2 | 1495 | DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61) |
| 565 | 566 | RXA00782 | GR00206 | 3984 | 3103 | SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5) |
| 567 | 568 | RXA00783 | GR00206 | 5280 | 4009 | SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5) |
| 569 | 570 | RXN01695 | VV0139 | 11307 | 12806 | L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16) |
| 571 | 572 | F RXA01615 | GR00449 | 8608 | 9546 | L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16) |
| 573 | 574 | F RXA01695 | GR00474 | 4388 | 4179 | L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16) |
| 575 | 576 | RXA00290 | GR00046 | 4693 | 5655 | MALIC ENZYME (EC 1.1.1.39) |
| 577 | 578 | RXN01048 | VV0079 | 12539 | 11316 | MALIC ENZYME (EC 1.1.1.39) |
| 579 | 580 | F RXA01048 | GR00296 | 3 | 290 | MALIC ENZYME (EC 1.1.1.39) |
| 581 | 582 | F RXA00290 | GR00046 | 4693 | 5655 | MALIC ENZYME (EC 1.1.1.39) |
| 583 | 584 | RXN03101 | VV0066 | 2 | 583 | DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61) |
| 585 | 586 | RXN02046 | VV0025 | 15056 | 14640 | DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61) |
| 587 | 588 | RXN00389 | VV0025 | 11481 | 9922 | oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-) |

Glyoxylate bypass

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|-------------------------------|
| 589 | 590 | RXN02399 | VV0176 | 19708 | 18365 | ISOCITRATE LYASE (EC 4.1.3.1) |
| 591 | 592 | F RXA02399 | GR00699 | 478 | 1773 | ISOCITRATE LYASE (EC 4.1.3.1) |
| 593 | 594 | RXN02404 | VV0176 | 20259 | 22475 | MALATE SYNTHASE (EC 4.1.3.2) |
| 595 | 596 | F RXA02404 | GR00700 | 3798 | 1663 | MALATE SYNTHASE (EC 4.1.3.2) |
| 597 | 598 | RXA01089 | GR00304 | 3209 | 3958 | GLYOXYLATE-INDUCED PROTEIN |
| 599 | 600 | RXA01886 | GR00539 | 3203 | 2430 | GLYOXYLATE-INDUCED PROTEIN |

Methylcitrate-pathway

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 601 | 602 | RXN03117 | VV0092 | 3087 | 1576 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 603 | 604 | F RXA00406 | GR00090 | 978 | 4 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 605 | 606 | F RXA00514 | GR00130 | 1983 | 1576 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 607 | 608 | RXA00512 | GR00130 | 621 | 4 | 2-methylcitrate synthase (EC 4.1.3.31) |
| 609 | 610 | RXA00518 | GR00131 | 3069 | 2773 | 2-methylcitrate synthase (EC 4.1.3.31) |
| 611 | 612 | RXA01077 | GR00300 | 4647 | 6017 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 613 | 614 | RXN03144 | VV0141 | 2 | 901 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 615 | 616 | F RXA02322 | GR00668 | 415 | 5 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 617 | 618 | RXA02329 | GR00669 | 607 | 5 | 2-methylisocitrate synthase (EC 5.3.3.-) |
| 619 | 620 | RXA02332 | GR00671 | 1906 | 764 | 2-methylcitrate synthase (EC 4.1.3.31) |
| 621 | 622 | RXN02333 | VV0141 | 901 | 1815 | methylisocitrate lyase (EC 4.1.3.30) |
| 623 | 624 | F RXA02333 | GR00671 | 2120 | 1902 | methylisocitrate lyase (EC 4.1.3.30) |
| 625 | 626 | RXA00030 | GR00003 | 9590 | 9979 | LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) |

Methyl-Malonyl-CoA-Mutases

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 627 | 628 | RXN00148 | VV0167 | 9849 | 12059 | METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2) |
| 629 | 630 | F RXA00148 | GR00023 | 2002 | 5 | METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2) |
| 631 | 632 | RXA00149 | GR00023 | 3856 | 2009 | METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2) |

Others

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|--|
| 633 | 634 | RXN00317 | VV0197 | 26879 | 27532 | PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18) |
| 635 | 636 | F RXA00317 | GR00055 | 344 | 6 | PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18) |
| 637 | 638 | RXA02196 | GR00645 | 3956 | 3264 | PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18) |
| 639 | 640 | RXN02461 | VV0124 | 14236 | 14643 | PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18) |

Redox Chain

| <u>Nucleic Acid</u> <u>SEQ ID NO</u> | <u>Amino Acid</u> <u>SEQ ID NO</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---|---------------------------------------|----------------------------|----------------|-----------------|----------------|---|
| 641 | 642 | RXN01744 | VV0174 | 2350 | 812 | CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-) |
| 643 | 644 | F RXA00055 | GR00008 | 11753 | 11890 | CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-) |
| 645 | 646 | F RXA01744 | GR00494 | 2113 | 812 | CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-) |
| 647 | 648 | RXA00379 | GR00082 | 212 | 6 | CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA |
| 649 | 650 | RXA00385 | GR00083 | 773 | 435 | CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA |
| 651 | 652 | RXA01743 | GR00494 | 806 | 6 | CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-) |
| 653 | 654 | RXN02480 | VV0084 | 31222 | 29567 | CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) |
| 655 | 656 | F RXA01919 | GR00550 | 288 | 4 | CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1) |
| 657 | 658 | F RXA02480 | GR00717 | 1449 | 601 | CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) |
| 659 | 660 | F RXA02481 | GR00717 | 1945 | 1334 | CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) |
| 661 | 662 | RXA02140 | GR00639 | 7339 | 8415 | CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) |
| 663 | 664 | RXA02142 | GR00639 | 9413 | 10063 | CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) |
| 665 | 666 | RXA02144 | GR00639 | 11025 | 12248 | CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) |
| 667 | 668 | RXA02740 | GR00763 | 7613 | 8542 | PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR |
| 669 | 670 | RXA02743 | GR00763 | 13534 | 12497 | CYTOCHROME AA3 CONTROLLING PROTEIN |
| 671 | 672 | RXA01227 | GR00355 | 1199 | 1519 | FERREDOXIN |
| 673 | 674 | RXA01865 | GR00532 | 436 | 122 | FERREDOXIN |
| 675 | 676 | RXA00680 | GR00179 | 2632 | 2315 | FERREDOXIN VI |
| 677 | 678 | RXA00679 | GR00179 | 2302 | 1037 | FERREDOXIN--NAD(+) REDUCTASE (EC 1.18.1.3) |
| 679 | 680 | RXA00224 | GR00032 | 24965 | 24015 | ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT |
| 681 | 682 | RXA00225 | GR00032 | 25783 | 24998 | ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT |
| 683 | 684 | RXN00606 | VV0192 | 11299 | 9026 | NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3) |
| 685 | 686 | F RXA00606 | GR00160 | 121 | 1869 | NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3) |
| 687 | 688 | RXN00595 | VV0192 | 8642 | 7113 | NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3) |
| 689 | 690 | F RXA00608 | GR00160 | 2253 | 3017 | NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3) |
| 691 | 692 | RXA00913 | GR00249 | 3 | 2120 | NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3) |
| 693 | 694 | RXA00909 | GR00247 | 2552 | 3406 | NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3) |
| 695 | 696 | RXA00700 | GR00182 | 846 | 43 | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 |
| 697 | 698 | RXN00483 | VV0086 | 44824 | 46287 | NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) |
| 699 | 700 | F RXA00483 | GR00119 | 19106 | 20569 | NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) |
| 701 | 702 | RXA01534 | GR00427 | 1035 | 547 | NADH-DEPENDENT FMN OXYDOREDUCTASE |

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 703 | 704 | RXA00288 | GR00046 | 2646 | 1636 | QUINONE OXIDOREDUCTASE (EC 1.6.5.5) |
| 705 | 706 | RXA02741 | GR00763 | 9585 | 8620 | QUINONE OXIDOREDUCTASE (EC 1.6.5.5) |
| 707 | 708 | RXN02560 | VV0101 | 9922 | 10788 | NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-) |
| 709 | 710 | F RXA02560 | GR00731 | 6339 | 7160 | NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-) |
| 711 | 712 | RXA01311 | GR00380 | 1611 | 865 | SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1) |
| 713 | 714 | RXN03014 | VV0058 | 1273 | 368 | NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3) |
| 715 | 716 | F RXA00910 | GR00248 | 3 | 1259 | Hydrogenase subunits |
| 717 | 718 | RXN01895 | VV0117 | 955 | 5 | NADH DEHYDROGENASE (EC 1.6.99.3) |
| 719 | 720 | F RXA01895 | GR00543 | 2 | 817 | DEHYDROGENASE |
| 721 | 722 | RXA00703 | GR00183 | 2556 | 271 | FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2) |
| 723 | 724 | RXN00705 | VV0005 | 6111 | 5197 | FDHD PROTEIN |
| 725 | 726 | F RXA00705 | GR00184 | 1291 | 407 | FDHD PROTEIN |
| 727 | 728 | RXN00388 | VV0025 | 2081 | 3091 | CYTOCHROME C BIOGENESIS PROTEIN CCSA |
| 729 | 730 | F RXA00388 | GR00085 | 969 | 667 | essential protein similar to cytochrome c |
| 731 | 732 | F RXA00386 | GR00084 | 514 | 5 | RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein |
| 733 | 734 | RXA00945 | GR00259 | 1876 | 2847 | putative cytochrome oxidase |
| 735 | 736 | RXN02556 | VV0101 | 5602 | 6759 | FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7) |
| 737 | 738 | F RXA02556 | GR00731 | 2019 | 3176 | FLAVOHEMOPROTEIN |
| 739 | 740 | RXA01392 | GR00408 | 2297 | 3373 | GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) |
| 741 | 742 | RXA00800 | GR00214 | 2031 | 3134 | GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1) |
| 743 | 744 | RXA02143 | GR00639 | 10138 | 11025 | QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase |
| 745 | 746 | RXN03096 | VV0058 | 405 | 4 | NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3) |
| 747 | 748 | RXN02036 | VV0176 | 32683 | 33063 | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) |
| 749 | 750 | RXN02765 | VV0317 | 3552 | 2794 | Hypothetical Oxidoreductase |
| 751 | 752 | RXN02206 | VV0302 | 1784 | 849 | Hypothetical Oxidoreductase |
| 753 | 754 | RXN02554 | VV0101 | 4633 | 4010 | Hypothetical Oxidoreductase (EC 1.1.1.-) |

ATP-Synthase

| Nucleic Acid SEQ ID NO | Amino Acid SEQ ID NO | Identification Code | Contig. | NT Start | NT Stop | Function |
|---------------------------|-------------------------|---------------------|---------|----------|---------|--|
| 755 | 756 | RXN01204 | VV0121 | 1270 | 461 | ATP SYNTHASE A CHAIN (EC 3.6.1.34) |
| 757 | 758 | F RXA01204 | GR00345 | 394 | 1155 | ATP SYNTHASE A CHAIN (EC 3.6.1.34) |
| 759 | 760 | RXA01201 | GR00344 | 675 | 2315 | ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34) |
| 761 | 762 | RXN01193 | VV0175 | 5280 | 3832 | ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) |
| 763 | 764 | F RXA01193 | GR00343 | 15 | 755 | ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) |
| 765 | 766 | F RXA01203 | GR00344 | 3355 | 3993 | ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) |
| 767 | 768 | RXN02821 | VV0121 | 324 | 85 | ATP SYNTHASE C CHAIN (EC 3.6.1.34) |
| 769 | 770 | F RXA02821 | GR00802 | 139 | 318 | ATP SYNTHASE C CHAIN (EC 3.6.1.34) |
| 771 | 772 | RXA01200 | GR00344 | 2 | 610 | ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34) |
| 773 | 774 | RXA01194 | GR00343 | 770 | 1141 | ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34) |

| <u>Nucleic Acid</u> | <u>Amino Acid</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---------------------|-------------------|----------------------------|----------------|-----------------|----------------|--|
| <u>SEQ ID NO</u> | <u>SEQ ID NO</u> | | | | | |
| 775 | 776 | RXA01202 | GR00344 | 2375 | 3349 | ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34) |
| 777 | 778 | RXN02434 | VW0090 | 4923 | 3274 | ATP-BINDING PROTEIN |

Cytochrome metabolism

| <u>Nucleic Acid</u> | <u>Amino Acid</u> | <u>Identification Code</u> | <u>Contig.</u> | <u>NT Start</u> | <u>NT Stop</u> | <u>Function</u> |
|---------------------|-------------------|----------------------------|----------------|-----------------|----------------|--|
| <u>SEQ ID NO</u> | <u>SEQ ID NO</u> | | | | | |
| 779 | 780 | RXN00684 | VW0005 | 29864 | 28581 | CYTOCHROME P450 116 (EC 1.14.-.-) |
| 781 | 782 | RXN00387 | VW0025 | 1150 | 2004 | Hypothetical Cytochrome c Biogenesis Protein |

TABLE 2: GENES IDENTIFIED FROM GENBANK

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---|------------------|--|--|
| A09073 | ppg | Phosphoenol pyruvate carboxylase | Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90 |
| A45579. A45581. A45583. A45585 A45587 | | Threonine dehydratase | Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95 |
| AB003132 | murC; ftsQ; ftsZ | | Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997) |
| AB015023 | murC; ftsQ | | Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999) |
| AB018530 | ftsR | | Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996) |
| AB018531 | ftsR1; ftsR2 | | |
| AB020624 | murI | D-glutamate racemase | |
| AB023377 | tki | transketolase | |
| AB024708 | gluB; gltD | Glutamine 2-oxoglutarate aminotransferase large and small subunits | |
| AB025424 | acn | aconitase | |
| AB027714 | rep | Replication protein | |
| AB027715 | rep; aad | Replication protein; aminoglycoside adenyltransferase | |
| AF005242 | argC | N-acetylglutamate-5-semialdehyde dehydrogenase | |
| AF005635 | glnA | Glutamine synthetase | |
| AF030405 | hisF | cyclase | |
| AF030520 | argG | Argininosuccinate synthetase | |
| AF031518 | argF | Ornithine carbamoyltransferase | |
| AF036932 | aroD | 3-dehydroquinate dehydratase | |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|--|---|--|
| AF038548 | pyc | Pyruvate carboxylase | Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998) |
| AF038651 | dcIAE; apt; rel | Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase | |
| AF041436 | argR | Arginine repressor | |
| AF045998 | impA | Inositol monophosphate phosphatase | |
| AF048764 | argH | Argininosuccinate lyase | |
| AF049897 | argC; argJ; argB; argD; argF; argR; argG; argH | N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase | |
| AF050109 | inhA | Enoyl-acyl carrier protein reductase | |
| AF050166 | hisG | ATP phosphoribosyltransferase | |
| AF051846 | hisA | Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase | Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998) |
| AF052652 | metA | Homoserine O-acetyltransferase | |
| AF053071 | aroB | Dehydroquinase synthetase | |
| AF060558 | hisH | Glutamine amidotransferase | |
| AF086704 | hisE | Phosphoribosyl-ATP-pyrophosphohydrolase | |
| AF114233 | aroA | 5-enolpyruvylshikimate 3-phosphate synthase | |
| AF116184 | panD | L-aspartate-alpha-decarboxylase precursor | |
| | | | Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|-----------------------------|---|--|
| AF124518 | aroD; aroE | 3-dehydroquinase; shikimate dehydrogenase | |
| AF124600 | aroC; aroK; aroB; pepQ | Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase | |
| AF145897 | inhA | | |
| AF145898 | inhA | | |
| AJ001436 | ectP | Transport of ectoine, glycine betaine, proline | Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998) |
| AJ004934 | dapD | Tetrahydrodipicolinate succinylase (incomplete) | Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998) |
| AJ007732 | ppc; secG; amt; ocd; soxA | Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase | |
| AJ010319 | ftsY, glnB, glnD; srp; amtP | Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein | Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999) |
| AJ132968 | cat | Chloramphenicol acetyl transferase | |
| AJ224946 | mgo | L-malate: quinone oxidoreductase | Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998) |
| AJ238250 | ndh | NADH dehydrogenase | |
| AJ238703 | porA | Porin | Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998) |
| D17429 | | Transposable element IS31831 | Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|------------|---|--|
| D84102 | odhA | 2-oxoglutarate dehydrogenase | Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996) |
| E01358 | hdh; hk | Homoserine dehydrogenase; homoserine kinase | Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87 |
| E01359 | | Upstream of the start codon of homoserine kinase gene | Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87 |
| E01375 | | Tryptophan operon | |
| E01376 | trpL; trpE | Leader peptide; anthranilate synthase | Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87 |
| E01377 | | Promoter and operator regions of tryptophan operon | Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87 |
| E03937 | | Biotin-synthase | Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92 |
| E04040 | | Diamino pelargonic acid aminotransferase | Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92 |
| E04041 | | Desthiobiotinsynthetase | Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92 |
| E04307 | | Flavum aspartase | Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93 |
| E04376 | | Isocitric acid lyase | Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93 |
| E04377 | | Isocitric acid lyase N-terminal fragment | Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93 |
| E04484 | | Prephenate dehydratase | Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93 |
| E05108 | | Aspartokinase | Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93 |
| E05112 | | Dihydro-dipichorinate synthetase | Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93 |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|--|-----------|--|---|
| E05776 | | Diaminopimelic acid dehydrogenase | Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93 |
| E05779 | | Threonine synthase | Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93 |
| E06110 | | Prephenate dehydratase | Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93 |
| E06111 | | Mutated Prephenate dehydratase | Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93 |
| E06146 | | Acetohydroxy acid synthetase | Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93 |
| E06825 | | Aspartokinase | Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94 |
| E06826 | | Mutated aspartokinase alpha subunit | Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94 |
| E06827 | | Mutated aspartokinase alpha subunit | Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94 |
| E07701 | secY | | Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94 |
| E08177 | | Aspartokinase | Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94 |
| E08178, E08179, E08180, E08181, E08182 | | Feedback inhibition-released Aspartokinase | Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94 |
| E08232 | | Acetohydroxy-acid isomeroreductase | Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94 |
| E08234 | secE | | Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94 |
| E08643 | | FT aminotransferase and desthiobiotin synthetase promoter region | Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95 |
| E08646 | | Biotin synthetase | Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95 |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------------|------------------|--|---|
| E08649 | | Aspartase | Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95 |
| E08900 | | Dihydrodipicolinate reductase | Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95 |
| E08901 | | Diaminopimelic acid decarboxylase | Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95 |
| E12594 | | Serine hydroxymethyltransferase | Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97 |
| E12760, E12759, E12758 | | transposase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12764 | | Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12767 | | Dihydrodipicolinic acid synthetase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12770 | | aspartokinase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E12773 | | Dihydrodipicolinic acid reductase | Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97 |
| E13655 | | Glucose-6-phosphate dehydrogenase | Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97 |
| L01508 | IlvA | Threonine dehydratase | Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992) |
| L07603 | EC 4.2.1.15 | 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase | Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993) |
| L09232 | IlvB; ilvN; ilvC | Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase | Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|-----------|--|--|
| L18874 | PtsM | Phosphoenolpyruvate sugar phosphotransferase | Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994) |
| L27123 | aceB | Malate synthase | Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994) |
| L27126 | | Pyruvate kinase | Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994) |
| L28760 | aceA | Isocitrate lyase | |
| L35906 | dtxr | Diphtheria toxin repressor | Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995) |
| M13774 | | Prephenate dehydratase | Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986) |
| M16175 | 5S rRNA | | Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987) |
| M16663 | trpE | Anthranilate synthase, 5' end | Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987) |
| M16664 | trpA | Tryptophan synthase, 3' end | Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987) |
| M25819 | | Phosphoenolpyruvate carboxylase | O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989) |
| M85106 | | 23S rRNA gene insertion sequence | Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|---------------------|--|---|
| M85107, M85108 | | 23S rRNA gene insertion sequence | Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992) |
| M89931 | aecD; brnQ; yhbW | Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW | Rosol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998) |
| S59299 | trp | Leader gene (promoter) | Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-producing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993) |
| U11545 | trpD | Anthranilate phosphoribosyltransferase | O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland. |
| U13922 | cgIM; cglIR; cglIIR | Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease | Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997) |
| U14965 | recA | | |
| U31224 | ppx | | Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996) |
| U31225 | proC | L-proline: NADP+ 5-oxidoreductase | Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996) |
| U31230 | obg; proB; unkdh | ?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases | Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|--|---|---|
| U31281 | bioB | Biotin synthase | Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996) |
| U35023 | thtR; accBC | Thiosulfate sulfurtransferase; acyl CoA carboxylase | Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996) |
| U43535 | cmr | Multidrug resistance protein | Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997) |
| U43536 | clpB | Heat shock ATP-binding protein | |
| U53587 | aphA-3 | 3'-5'-aminoglycoside phosphotransferase | |
| U89648 | | <i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence. | |
| X04960 | trpA; trpB; trpC; trpD; trpE; trpG; trpL | Tryptophan operon | Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986) |
| X07563 | lys A | DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20) | Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988) |
| X14234 | EC 4.1.1.31 | Phosphoenolpyruvate carboxylase | Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993) |
| X17313 | fda | Fructose-bisphosphate aldolase | Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> |
| X53993 | dapA | L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52) | Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|----------------------------|--|---|
| X54223 | | AttB-related site | Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990) |
| X54740 | argS; lysA | Arginyl-tRNA synthetase; Diaminopimelate decarboxylase | Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990) |
| X55994 | trpL; trpE | Putative leader peptide; anthranilate synthase component I | Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990) |
| X56037 | thrC | Threonine synthase | Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990) |
| X56075 | attB-related site | Attachment site | Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990) |
| X57226 | lysC-alpha; lysC-beta; asd | Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase | Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990) |
| X59403 | gap;pgk; tpi | Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase | Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992) |
| X59404 | gdh | Glutamate dehydrogenase | Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992) |
| X60312 | lysI | L-lysine permease | Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|------------|----------------------------------|---|
| X66078 | cop1 | Ps1 protein | Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992) |
| X66112 | glt | Citrate synthase | Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994) |
| X67737 | dapB | Dihydrodipicolinate reductase | |
| X69103 | csp2 | Surface layer protein PS2 | Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993) |
| X69104 | | IS3 related insertion element | Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994) |
| X70959 | leuA | Isopropylmalate synthase | Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994) |
| X71489 | icd | Isocitrate dehydrogenase (NADP+) | Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995) |
| X72855 | GDHA | Glutamate dehydrogenase (NADP+) | |
| X75083, X70584 | mttA | 5-methyltryptophan resistance | Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994) |
| X75085 | recA | | Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994) |
| X75504 | aceA; thiX | Partial Isocitrate lyase; ? | Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994) |
| X76875 | | ATPase beta-subunit | Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|---------------------------|---|--|
| X77034 | tuf | Elongation factor Tu | Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993) |
| X77384 | recA | | Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994) |
| X78491 | aceB | Malate synthase | Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994) |
| X80629 | 16S rDNA | 16S ribosomal RNA | Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995) |
| X81191 | gluA; gluB; gluC; gluD | Glutamate uptake system | Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995) |
| X81379 | dapE | Succinyldiaminopimelate desuccinylase | Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994) |
| X82061 | 16S rDNA | 16S ribosomal RNA | Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995) |
| X82928 | asd; lysC | Aspartate-semialdehyde dehydrogenase; ? | Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995) |
| X82929 | proA | Gamma-glutamyl phosphate reductase | Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995) |
| X84257 | 16S rDNA | 16S ribosomal RNA | Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995) |
| X85965 | aroP; dapE | Aromatic amino acid permease; ? | Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|---------------------------------|---|--|
| X86157 | argB; argC; argD; argF; argJ | Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase | Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996) |
| X89084 | pta; ackA | Phosphate acetyltransferase; acetate kinase | Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999) |
| X89850 | attB | Attachment site | Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996) |
| X90356 | | Promoter fragment F1 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90357 | | Promoter fragment F2 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90358 | | Promoter fragment F10 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90359 | | Promoter fragment F13 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90360 | | Promoter fragment F22 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90361 | | Promoter fragment F34 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90362 | | Promoter fragment F37 | Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|---------------------------|------------|--|---|
| X90363 | | Promoter fragment F45 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90364 | | Promoter fragment F64 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90365 | | Promoter fragment F75 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90366 | | Promoter fragment PF101 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90367 | | Promoter fragment PF104 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X90368 | | Promoter fragment PF109 | Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996) |
| X93513 | amt | Ammonium transport system | Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996) |
| X93514 | betP | Glycine betaine transport system | Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996) |
| X95649 | orf4 | | Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997) |
| X96471 | lysE, lysG | Lysine exporter protein; Lysine export regulator protein | Vrijic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|-----------------------|--|---|
| X96580 | panB; panC; xylB | 3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase | Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999) |
| X96962 | | Insertion sequence IS1207 and transposase | |
| X99289 | | Elongation factor P | Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997) |
| Y00140 | thrB | Homoserine kinase | Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987) |
| Y00151 | ddh | Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16) | Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987) |
| Y00476 | thrA | Homoserine dehydrogenase | Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987) |
| Y00546 | hom; thrB | Homoserine dehydrogenase; homoserine kinase | Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988) |
| Y08964 | murC; ftsQ/divD; ftsZ | UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein | Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998) |
| Y09163 | putP | High affinity proline transport system | Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997) |
| Y09548 | pyc | Pyruvate carboxylase | Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998) |
| Y09578 | leuB | 3-isopropylmalate dehydrogenase | Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998) |
| Y12472 | | Attachment site bacteriophage Phi-16 | Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999) |

| GenBank™ Accession No. | Gene Name | Gene Function | Reference |
|------------------------|------------|---|--|
| Y12537 | proP | Proline/ectoine uptake system protein | Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998) |
| Y13221 | glnA | Glutamine synthetase I | Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997) |
| Y16642 | lpd | Dihydrolipoamide dehydrogenase | |
| Y18059 | | Attachment site Corynebacterium 304L | Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999) |
| Z21501 | argS; lysA | Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial) | Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993) |
| Z21502 | dapA; dapB | Dihydrodipicolinate synthase; dihydrodipicolinate reductase | Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993) |
| Z29563 | thrC | Threonine synthase | Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994) |
| Z46753 | 16S rDNA | Gene for 16S ribosomal RNA | |
| Z49822 | sigA | SigA sigma factor | Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996) |
| Z49823 | galE; dtxR | Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein | Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996) |
| Z49824 | orf1; sigB | ?; SigB sigma factor | Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996) |
| Z66534 | | Transposase | Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996) |

¹ A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

| Genus | Species | ATCC | DSMZ | ERM | NRRL | CECT | NCIMB | CBS | NCIC | DSMZ |
|----------------|--------------|-------|------|------|--------|------|-------|-----|------|------|
| Brevibacterium | ammoniogenes | 21054 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19350 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19351 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19352 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19353 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19354 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19355 | | | | | | | | |
| Brevibacterium | ammoniogenes | 19356 | | | | | | | | |
| Brevibacterium | ammoniogenes | 21055 | | | | | | | | |
| Brevibacterium | ammoniogenes | 21077 | | | | | | | | |
| Brevibacterium | ammoniogenes | 21553 | | | | | | | | |
| Brevibacterium | ammoniogenes | 21580 | | | | | | | | |
| Brevibacterium | ammoniogenes | 39101 | | | | | | | | |
| Brevibacterium | butanicum | 21196 | | | | | | | | |
| Brevibacterium | divaricatum | 21792 | | P928 | | | | | | |
| Brevibacterium | flavum | 21474 | | | | | | | | |
| Brevibacterium | flavum | 21129 | | | | | | | | |
| Brevibacterium | flavum | 21518 | | | | | | | | |
| Brevibacterium | flavum | | | | B11474 | | | | | |
| Brevibacterium | flavum | | | | B11472 | | | | | |
| Brevibacterium | flavum | 21127 | | | | | | | | |
| Brevibacterium | flavum | 21128 | | | | | | | | |
| Brevibacterium | flavum | 21427 | | | | | | | | |
| Brevibacterium | flavum | 21475 | | | | | | | | |
| Brevibacterium | flavum | 21517 | | | | | | | | |
| Brevibacterium | flavum | 21528 | | | | | | | | |
| Brevibacterium | flavum | 21529 | | | | | | | | |

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|----------------|------------------|-------|--|--------|-------|--------|--|--|--|
| Brevibacterium | flavum | | | B11477 | | | | | |
| Brevibacterium | flavum | | | B11478 | | | | | |
| Brevibacterium | flavum | 21127 | | | | | | | |
| Brevibacterium | flavum | | | B11474 | | | | | |
| Brevibacterium | healii | 15527 | | | | | | | |
| Brevibacterium | ketoglutamicum | 21004 | | | | | | | |
| Brevibacterium | ketoglutamicum | 21089 | | | | | | | |
| Brevibacterium | ketosoreductum | 21914 | | | | | | | |
| Brevibacterium | lactofermentum | | | | 70 | | | | |
| Brevibacterium | lactofermentum | | | | 74 | | | | |
| Brevibacterium | lactofermentum | | | | 77 | | | | |
| Brevibacterium | lactofermentum | 21798 | | | | | | | |
| Brevibacterium | lactofermentum | 21799 | | | | | | | |
| Brevibacterium | lactofermentum | 21800 | | | | | | | |
| Brevibacterium | lactofermentum | 21801 | | | | | | | |
| Brevibacterium | lactofermentum | | | B11470 | | | | | |
| Brevibacterium | lactofermentum | | | B11471 | | | | | |
| Brevibacterium | lactofermentum | 21086 | | | | | | | |
| Brevibacterium | lactofermentum | 21420 | | | | | | | |
| Brevibacterium | lactofermentum | 21086 | | | | | | | |
| Brevibacterium | lactofermentum | 31269 | | | | | | | |
| Brevibacterium | linens | 9174 | | | | | | | |
| Brevibacterium | linens | 19391 | | | | | | | |
| Brevibacterium | linens | 8377 | | | | | | | |
| Brevibacterium | paraffinolyticum | | | | 11160 | | | | |
| Brevibacterium | spec. | | | | | 717.73 | | | |
| Brevibacterium | spec. | | | | | 717.73 | | | |
| Brevibacterium | spec. | 14604 | | | | | | | |
| Brevibacterium | spec. | 21860 | | | | | | | |
| Brevibacterium | spec. | 21864 | | | | | | | |
| Brevibacterium | spec. | 21865 | | | | | | | |

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|-----------------|------------------|-------|--|--------|--|--|--|------|--|
| Brevibacterium | spec. | 21866 | | | | | | | |
| Brevibacterium | spec. | 19240 | | | | | | | |
| Corynebacterium | acetoacidophilum | 21476 | | | | | | | |
| Corynebacterium | acetoacidophilum | 13870 | | | | | | | |
| Corynebacterium | acetoglutamicum | | | B11473 | | | | | |
| Corynebacterium | acetoglutamicum | | | B11475 | | | | | |
| Corynebacterium | acetoglutamicum | 15806 | | | | | | | |
| Corynebacterium | acetoglutamicum | 21491 | | | | | | | |
| Corynebacterium | acetoglutamicum | 31270 | | | | | | | |
| Corynebacterium | acetophilum | | | B3671 | | | | | |
| Corynebacterium | ammoniaenes | 6872 | | | | | | 2399 | |
| Corynebacterium | ammoniaenes | 15511 | | | | | | | |
| Corynebacterium | fujikense | 21496 | | | | | | | |
| Corynebacterium | glutamicum | 14067 | | | | | | | |
| Corynebacterium | glutamicum | 39137 | | | | | | | |
| Corynebacterium | glutamicum | 21254 | | | | | | | |
| Corynebacterium | glutamicum | 21255 | | | | | | | |
| Corynebacterium | glutamicum | 31830 | | | | | | | |
| Corynebacterium | glutamicum | 13032 | | | | | | | |
| Corynebacterium | glutamicum | 14305 | | | | | | | |
| Corynebacterium | glutamicum | 15455 | | | | | | | |
| Corynebacterium | glutamicum | 13058 | | | | | | | |
| Corynebacterium | glutamicum | 13059 | | | | | | | |
| Corynebacterium | glutamicum | 13060 | | | | | | | |
| Corynebacterium | glutamicum | 21492 | | | | | | | |
| Corynebacterium | glutamicum | 21513 | | | | | | | |
| Corynebacterium | glutamicum | 21526 | | | | | | | |
| Corynebacterium | glutamicum | 21543 | | | | | | | |
| Corynebacterium | glutamicum | 13287 | | | | | | | |
| Corynebacterium | glutamicum | 21851 | | | | | | | |
| Corynebacterium | glutamicum | 21253 | | | | | | | |

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|-----------------|------------|-------|--|--|--|--|--|--|--|
| Corynebacterium | glutamicum | 21514 | | | | | | | |
| Corynebacterium | glutamicum | 21516 | | | | | | | |
| Corynebacterium | glutamicum | 21299 | | | | | | | |
| Corynebacterium | glutamicum | 21300 | | | | | | | |
| Corynebacterium | glutamicum | 39684 | | | | | | | |
| Corynebacterium | glutamicum | 21488 | | | | | | | |
| Corynebacterium | glutamicum | 21649 | | | | | | | |
| Corynebacterium | glutamicum | 21650 | | | | | | | |
| Corynebacterium | glutamicum | 19223 | | | | | | | |
| Corynebacterium | glutamicum | 13869 | | | | | | | |
| Corynebacterium | glutamicum | 21157 | | | | | | | |
| Corynebacterium | glutamicum | 21158 | | | | | | | |
| Corynebacterium | glutamicum | 21159 | | | | | | | |
| Corynebacterium | glutamicum | 21355 | | | | | | | |
| Corynebacterium | glutamicum | 31808 | | | | | | | |
| Corynebacterium | glutamicum | 21674 | | | | | | | |
| Corynebacterium | glutamicum | 21562 | | | | | | | |
| Corynebacterium | glutamicum | 21563 | | | | | | | |
| Corynebacterium | glutamicum | 21564 | | | | | | | |
| Corynebacterium | glutamicum | 21565 | | | | | | | |
| Corynebacterium | glutamicum | 21566 | | | | | | | |
| Corynebacterium | glutamicum | 21567 | | | | | | | |
| Corynebacterium | glutamicum | 21568 | | | | | | | |
| Corynebacterium | glutamicum | 21569 | | | | | | | |
| Corynebacterium | glutamicum | 21570 | | | | | | | |
| Corynebacterium | glutamicum | 21571 | | | | | | | |
| Corynebacterium | glutamicum | 21572 | | | | | | | |
| Corynebacterium | glutamicum | 21573 | | | | | | | |
| Corynebacterium | glutamicum | 21579 | | | | | | | |
| Corynebacterium | glutamicum | 19049 | | | | | | | |
| Corynebacterium | glutamicum | 19050 | | | | | | | |

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|-----------------|---------------|-------|--|--|-------|--------|--|-------|--|
| Corynebacterium | glutamicum | 19051 | | | | | | | |
| Corynebacterium | glutamicum | 19052 | | | | | | | |
| Corynebacterium | glutamicum | 19053 | | | | | | | |
| Corynebacterium | glutamicum | 19054 | | | | | | | |
| Corynebacterium | glutamicum | 19055 | | | | | | | |
| Corynebacterium | glutamicum | 19056 | | | | | | | |
| Corynebacterium | glutamicum | 19057 | | | | | | | |
| Corynebacterium | glutamicum | 19058 | | | | | | | |
| Corynebacterium | glutamicum | 19059 | | | | | | | |
| Corynebacterium | glutamicum | 19060 | | | | | | | |
| Corynebacterium | glutamicum | 19185 | | | | | | | |
| Corynebacterium | glutamicum | 13286 | | | | | | | |
| Corynebacterium | glutamicum | 21515 | | | | | | | |
| Corynebacterium | glutamicum | 21527 | | | | | | | |
| Corynebacterium | glutamicum | 21544 | | | | | | | |
| Corynebacterium | glutamicum | 21492 | | | | | | | |
| Corynebacterium | glutamicum | | | | | B8183 | | | |
| Corynebacterium | glutamicum | | | | | B8182 | | | |
| Corynebacterium | glutamicum | | | | | B12416 | | | |
| Corynebacterium | glutamicum | | | | | B12417 | | | |
| Corynebacterium | glutamicum | | | | | B12418 | | | |
| Corynebacterium | glutamicum | | | | | B11476 | | | |
| Corynebacterium | glutamicum | 21608 | | | | | | | |
| Corynebacterium | lilium | | | | P973 | | | | |
| Corynebacterium | nitrilophilus | 21419 | | | | | | 11594 | |
| Corynebacterium | spec. | | | | P4445 | | | | |
| Corynebacterium | spec. | | | | P4446 | | | | |
| Corynebacterium | spec. | 31088 | | | | | | | |
| Corynebacterium | spec. | 31089 | | | | | | | |
| Corynebacterium | spec. | 31090 | | | | | | | |
| Corynebacterium | spec. | 31090 | | | | | | | |

TABLE 4: ALIGNMENT RESULTS

| ID # | length (NT) | Genbank Hit | Length | Accession | Name of Genbank Hit | Source of Genbank Hit | % homology (GAP) | Date of Deposit |
|---------|----------------|-------------------|--------|-----------|---|----------------------------|---------------------|-----------------------------------|
| rx00013 | 996 | GB_GSS4:AQ713475 | 581 | AQ713475 | HS_5402_B2_A12_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence. | Homo sapiens | 37,148 | 13-Jul-99 |
| | | GB_HTG3:AC007420 | 130583 | AC007420 | Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPC1-88 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 83 unordered pieces. | Drosophila melanogaster | 34,568 | 20-Sep-99 |
| | | GB_HTG3:AC007420 | 130583 | AC007420 | Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPC1-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***; 83 unordered pieces. | Drosophila melanogaster | 34,568 | 20-Sep-99 |
| rx00014 | 903 | GB_BA1:MTCY3A2 | 25830 | Z83867 | Mycobacterium tuberculosis H37Rv complete genome; segment 136/162. | Mycobacterium tuberculosis | 58,140 | 17-Jun-98 |
| | | GB_BA1:MLCB1779 | 43254 | Z98271 | Mycobacterium leprae cosmid B1779. | Mycobacterium leprae | 57,589 | 8-Aug-97 |
| | | GB_BA1:SAPURCLUS | 9120 | X92429 | S.alboniger naph, pur7, pur10, pur6, pur4, pur5 and pur3 genes. | Streptomyces anulatus | 55,667 | 28-Feb-96 |
| rx00030 | 513 | GB_EST21:C89713 | 767 | C89713 | C89713 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence. | Dictyostelium discoideum | 45,283 | 20-Apr-98 |
| | | GB_EST28:A1497294 | 484 | A1497294 | fb63g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOC P80961 ANTIFREEZE PROTEIN LS-12.; mRNA sequence. | Danio rerio | 42,991 | 11-MAR-1999 |
| | | GB_EST21:C92167 | 637 | C92167 | C92167 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence. | Dictyostelium discoideum | 44,444 | 12-Jul-99 |
| rx00032 | 1632 | GB_BA2:AF010496 | 189370 | AF010496 | Rhodobacter capsulatus strain SB1003, partial genome. | Rhodobacter capsulatus | 39,689 | 12-MAY-1998 |
| | | GB_BA2:AF018073 | 9810 | AF018073 | Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtiK), and periplasmic mannitol-binding protein (smoM) genes, complete cds. | Rhodobacter sphaeroides | 48,045 | 22-OCT-1997 |
| rx00041 | 1342 | GB_BA2:AF045245 | 5930 | AF045245 | Klebsiella pneumoniae D-arabinitol transporter (dalT), D-arabinitol kinase (dalK), D-arabinitol dehydrogenase (dalD), and repressor (dalR) genes, complete cds. | Klebsiella pneumoniae | 38,514 | 16-Jul-98 |
| | | EM_PAT:E11760 | 6911 | E11760 | Base sequence of sucrose gene. | Corynebacterium glutamicum | 99,031 | 08-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:I26124 | 6911 | I26124 | Sequence 4 from patent US 5556776. | Unknown. | 99,031 | 07-OCT-1996 |
| | | GB_IN1:LMFL5883 | 31934 | AL117384 | Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence. | Leishmania major | 43,663 | 21-OCT-1999 |
| rx00042 | 882 | EM_PAT:E11760 | 6911 | E11760 | Base sequence of sucrose gene. | Corynebacterium glutamicum | 94,767 | 08-OCT-1997 (Rel. 52, Created) |
| | | GB_PAT:I26124 | 6911 | I26124 | Sequence 4 from patent US 5556776. | Unknown. | 94,767 | 07-OCT-1996 |
| | | GB_IN1:CEU33051 | 4899 | U33051 | Caenorhabditis elegans sur-2 mRNA, complete cds. | Caenorhabditis elegans | 40,276 | 23-Jan-96 |
| rx00043 | 1287 | GB_PAT:I26124 | 6911 | I26124 | Sequence 4 from patent US 5556776. | Unknown. | 97,591 | 07-OCT-1996 |
| | | EM_PAT:E11760 | 6911 | E11760 | Base sequence of sucrose gene. | Corynebacterium glutamicum | 97,591 | 08-OCT-1997 (Rel. 52, Created) |
| | | GB_PR3:AC005174 | 39769 | AC005174 | Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence. | Homo sapiens | 35,879 | 24-Jun-88 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|-------------------------------|--------|-------------|
| rx00098 | 1743 | GB_BA1:MSU88433 | 1928 | U88433 | Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds. | Mycobacterium smegmatis | 62,658 | 19-Apr-97 |
| | | GB_BA1:SC5A7 | 40337 | AL031107 | Streptomyces coelicolor cosmid 5A7. | Streptomyces coelicolor | 37,638 | 27-Jul-98 |
| | | GB_BA1:MTCY10D7 | 39800 | Z79700 | Mycobacterium tuberculosis H37Rv complete genome; segment 44/162. | Mycobacterium tuberculosis | 36,784 | 17-Jun-98 |
| rx00148 | 2334 | GB_BA1:MTCY277 | 38300 | Z79701 | Mycobacterium tuberculosis H37Rv complete genome; segment 65/162. | Mycobacterium tuberculosis | 67,457 | 17-Jun-98 |
| | | GB_BA1:MSGY456 | 37316 | AD000001 | Mycobacterium tuberculosis sequence from clone y456. | Mycobacterium tuberculosis | 40,883 | 03-DEC-1996 |
| | | GB_BA1:MSGY175 | 18106 | AD000015 | Mycobacterium tuberculosis sequence from clone y175. | Mycobacterium tuberculosis | 67,457 | 10-DEC-1996 |
| rx00149 | 1971 | GB_BA1:MSGY456 | 37316 | AD000001 | Mycobacterium tuberculosis sequence from clone y456. | Mycobacterium tuberculosis | 35,883 | 03-DEC-1996 |
| | | GB_BA1:MSGY175 | 18106 | AD000015 | Mycobacterium tuberculosis sequence from clone y175. | Mycobacterium tuberculosis | 51,001 | 10-DEC-1996 |
| | | GB_BA1:MTCY277 | 38300 | Z79701 | Mycobacterium tuberculosis H37Rv complete genome; segment 65/162. | Mycobacterium tuberculosis | 51,001 | 17-Jun-98 |
| rx00195 | 684 | GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 35,735 | 19-Jun-98 |
| | | GB_BA1:MSGY1528CS | 36985 | L78824 | Mycobacterium leprae cosmid B1529 DNA sequence. | Mycobacterium leprae | 57,014 | 15-Jun-96 |
| | | GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 41,892 | 19-Jun-98 |
| rx00196 | 738 | GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 41,841 | 19-Jun-98 |
| | | GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 36,599 | 19-Jun-98 |
| | | GB_RO:RATCBRQ | 10752 | M55532 | Rat carbohydrate binding receptor gene, complete cds. | Rattus norvegicus | 36,212 | 27-Apr-93 |
| rx00202 | 1065 | GB_EST11:AA253618 | 313 | AA253618 | mw95c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:678450 5', mRNA sequence. | Mus musculus | 38,816 | 13-MAR-1997 |
| | | GB_EST26:AI390284 | 490 | AI390284 | mw96a03.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:678508 5' similar to TR:O09171 O09171 BETAIN-HOMOCYSTEINE | Mus musculus | 42,239 | 2-Feb-99 |
| | | GB_EST26:AI390280 | 467 | AI390280 | METHYLTRANSFERASE,, mRNA sequence. | Mus musculus | 37,307 | 2-Feb-99 |
| | | GB_BA1:MLCB637 | 44882 | Z99263 | Mycobacterium leprae cosmid B637. | Mycobacterium leprae | 58,312 | 17-Sep-97 |
| rx00206 | 1161 | GB_BA1:MTV012 | 70287 | AL021287 | Mycobacterium tuberculosis H37Rv complete genome; segment 132/162. | Mycobacterium tuberculosis | 36,632 | 23-Jun-99 |
| | | GB_BA1:SC6E10 | 23990 | AL109661 | Streptomyces coelicolor cosmid 6E10. | Streptomyces coelicolor A3(2) | 38,616 | 5-Aug-99 |
| rx00224 | 1074 | GB_BA1:BUJ32230 | 1769 | U32230 | Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large Bradyrhizobium japonicum subunit (etfL) genes, complete cds. | Bradyrhizobium japonicum | 48,038 | 25-MAY-1996 |
| | | GB_BA1:PDEETFAB | 2440 | L14864 | Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's. | Paracoccus denitrificans | 48,351 | 27-OCT-1993 |
| | | GB_HTG3:AC009689 | 177954 | AC009689 | Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING. | Homo sapiens | 38,756 | 28-Aug-99 |
| rx00225 | 909 | GB_RO:AF060178 | 2057 | AF060178 | Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds. | Mus musculus | 39,506 | 18-Jun-98 |
| | | GB_GSS11:AQ325043 | 734 | AQ325043 | mgxb0020J01r CUGI Rice Blast Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence. | Magnaporthe grisea | 38,333 | 8-Jan-99 |
| | | GB_EST31:AI676413 | 551 | AI676413 | eimEST0167 EIH1 Eimeria tenella cDNA clone eimc074 5', mRNA sequence. | Eimeria tenella | 35,542 | 19-MAY-1999 |
| rx00235 | 1398 | GB_BA1:MTCY10G2 | 38970 | Z92539 | Mycobacterium tuberculosis H37Rv complete genome; segment 47/162. | Mycobacterium tuberculosis | 65,759 | 17-Jun-98 |
| | | GB_BA2:AF061753 | 3721 | AF061753 | Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds; and enolase (eno) gene, complete cds. | Nitrosomonas europaea | 58,941 | 31-Aug-98 |
| | | GB_BA2:AF086791 | 37867 | AF086791 | Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and exonuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes. | Zymomonas mobilis | 61,239 | 4-Nov-98 |
| rx00246 | 1158 | GB_BA2:AF012550 | 2690 | AF012550 | Acinetobacter sp. BD413 Comp (comp) gene, complete cds. | Acinetobacter sp. BD413 | 53,726 | 27-Sep-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|------------------|--------|-------------------|--------|----------|---|-----------------------------|--------|-------------|
| rx00251 | 831 | GB_PAT:E03856 | 1506 | E03856 | gDNA encoding alcohol dehydrogenase. | Bacillus stearothermophilus | 51,688 | 29-Sep-97 |
| | | GB_BA1:BACADHT | 1688 | D90421 | B.stearothermophilus adhT gene for alcohol dehydrogenase. | Bacillus stearothermophilus | 51,602 | 7-Feb-99 |
| | | GB_BA1:MTCY20G9 | 37218 | Z77162 | Mycobacterium tuberculosis H37Rv complete genome; segment 25/162. | Mycobacterium tuberculosis | 42,875 | 17-Jun-98 |
| | | GB_BA1:MTV004 | 69350 | AL009198 | Mycobacterium tuberculosis H37Rv complete genome; segment 144/162. | Mycobacterium tuberculosis | 40,380 | 18-Jun-98 |
| | | GB_BA1:MTV004 | 69350 | AL009198 | Mycobacterium tuberculosis H37Rv complete genome; segment 144/162. | Mycobacterium tuberculosis | 41,789 | 18-Jun-98 |
| rx00288 | 1134 | GB_BA2:AF050114 | 1038 | AF050114 | Pseudomonas sp. W7 alginate lyase gene, complete cds. | Pseudomonas sp. W7 | 49,898 | 03-MAR-1999 |
| | | GB_GSS3:B16984 | 469 | B16984 | 344A14.TVC C1978SKA1 Homo sapiens genomic clone A-344A14, genomic survey | Homo sapiens | 39,355 | 4-Jun-98 |
| | | | | | sequence. | | | |
| rx00293 | 1035 | GB_IN2:AF144549 | 7887 | AF144549 | Aedes albopictus ribosomal protein L34 (rpL34) gene, complete cds. | Aedes albopictus | 36,509 | 3-Jun-99 |
| | | GB_EST1:T28483 | 313 | T28483 | EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monoxygenase 1 (HT-1956), mRNA sequence. | Homo sapiens | 42,997 | 6-Sep-95 |
| | | GB_PRI1:HUMFMO1 | 2134 | M64082 | Human flavin-containing monoxygenase (FMO1) mRNA, complete cds. | Homo sapiens | 37,915 | 8-Nov-94 |
| | | GB_EST32:A1734238 | 512 | A1734238 | zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN), mRNA sequence. | Homo sapiens | 41,502 | 14-Jun-99 |
| rx00296 | 2967 | GB_HTG6:AC011069 | 168266 | AC011069 | Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 | Drosophila melanogaster | 33,890 | 02-DEC-1999 |
| | | | | | 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** | | | |
| | | | | | 92 unordered pieces. | | | |
| | | GB_EST15:AA531468 | 414 | AA531468 | nj63d12.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997175, mRNA sequence. | Homo sapiens | 40,821 | 20-Aug-97 |
| GB_HTG6:AC011069 | 168266 | AC011069 | | | Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 | Drosophila melanogaster | 30,963 | 02-DEC-1999 |
| | | | | | 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** | | | |
| | | | | | 92 unordered pieces. | | | |
| rx00310 | 558 | GB_VI:VMVY16780 | 186986 | Y16780 | variola minor virus complete genome. | variola minor virus | 35,883 | 2-Sep-99 |
| | | GB_VI:VARCG | 186103 | L22579 | Variola major virus (strain Bangladesh-1975) complete genome. | Variola major virus | 34,664 | 12-Jan-95 |
| | | GB_VI:VVCAG | 185578 | X69198 | Variola virus DNA complete genome. | Variola virus | 36,000 | 13-DEC-1996 |
| rx00317 | 777 | GB_HTG3:AC009571 | 159648 | AC009571 | Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS *** | Homo sapiens | 36,988 | 29-Sep-99 |
| | | | | | 8 unordered pieces. | | | |
| | | GB_HTG3:AC009571 | 159648 | AC009571 | Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS *** | Homo sapiens | 36,988 | 29-Sep-99 |
| | | | | | 8 unordered pieces. | | | |
| GB_PR3:AC005697 | 174503 | AC005697 | | | Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence. | Homo sapiens | 36,340 | 09-OCT-1998 |
| GB_BA1:LCATPASEB | 1514 | X64542 | | | L.casei gene for ATPase beta-subunit. | Lactobacillus casei | 34,664 | 11-DEC-1992 |
| GB_BA1:LCATPASEB | 1514 | X64542 | | | L.casei gene for ATPase beta-subunit. | Lactobacillus casei | 39,308 | 11-DEC-1992 |
| rx00328 | 615 | GB_BA1:STYPUTPE | 1887 | L01138 | Salmonella (S2980) proline permease (putP) gene, 5' end. | Salmonella sp. | 39,623 | 09-MAY-1996 |
| | | GB_BA1:STYPUTPF | 1887 | L01139 | Salmonella (S2983) proline permease (putP) gene, 5' end. | Salmonella sp. | 39,623 | 09-MAY-1996 |
| | | GB_BA1:STYPUTPI | 1889 | L01142 | Salmonella (S3015) proline permease (putP) gene, 5' end. | Salmonella sp. | 42,906 | 09-MAY-1996 |
| rx00329 | 1347 | GB_PR3:AC004691 | 141990 | AC004691 | Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. | Homo sapiens | 38,142 | 16-MAY-1998 |
| | | GB_PR4:AC004916 | 129014 | AC004916 | Homo sapiens clone DJ0891L14, complete sequence. | Homo sapiens | 38,549 | 17-Jul-99 |
| | | GB_PR3:AC004691 | 141990 | AC004691 | Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. | Homo sapiens | 35,865 | 16-MAY-1998 |
| rx00340 | 1269 | GB_BA1:MTCY427 | 38110 | Z70692 | Mycobacterium tuberculosis H37Rv complete genome; segment 99/162. | Mycobacterium tuberculosis | 38,940 | 24-Jun-99 |
| | | GB_GSS12:AQ412290 | 238 | AQ412290 | RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence. | Homo sapiens | 36,555 | 23-MAR-1999 |
| | | | | | | | | |
| | | GB_PL2:AF112871 | 2394 | AF112871 | Astasia longa small subunit ribosomal RNA gene, complete sequence. | Astasia longa | 36,465 | 28-Jun-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|------------------------------------|--------|-------------|
| rx00379 | 307 | GB_HTG1:CEY56A3 | 224746 | AL022280 | Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Caenorhabditis elegans | 35,179 | 6-Sep-99 |
| | | GB_HTG1:CEY56A3 | 224746 | AL022280 | Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Caenorhabditis elegans | 35,179 | 6-Sep-99 |
| | | GB_PR2:HS134O19 | 86897 | AL034555 | Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence. | Homo sapiens | 40,604 | 23-Nov-99 |
| rx00381 | 729 | GB_GSS4:AQ730532 | 416 | AQ730532 | HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence. | Homo sapiens | 35,766 | 15-Jul-99 |
| | | GB_EST23:AI120939 | 561 | AI120939 | ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:IM19381 Mouse calmodulin (MOUSE); mRNA sequence. | Mus musculus | 41,113 | 2-Sep-98 |
| | | GB_EST23:AI120939 | 561 | AI120939 | ub74f05.r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:IM19381 Mouse calmodulin (MOUSE); mRNA sequence. | Mus musculus | 41,113 | 2-Sep-98 |
| rx00385 | 362 | GB_EST32:AI726450 | 565 | AI726450 | BNLGH5857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence. | Gossypium hirsutum | 41,152 | 11-Jun-99 |
| | | GB_GSS4:AQ740856 | 768 | AQ740856 | HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence. | Homo sapiens | 41,360 | 16-Jul-99 |
| | | GB_PR1:HSPAIP | 1587 | X91809 | H.sapiens mRNA for GAIP protein. | Homo sapiens | 36,792 | 29-MAR-1996 |
| rx00388 | 1134 | GB_BA1:MTY13D10 | 40838 | Z95558 | Mycobacterium tuberculosis H37Rv complete genome; segment 28/162. | Mycobacterium tuberculosis | 51,852 | 17-Jun-98 |
| | | GB_BA1:MSGY224 | 40051 | AD000004 | Mycobacterium tuberculosis sequence from clone y224. | Mycobacterium tuberculosis | 51,852 | 03-DEC-1996 |
| | | GB_HTG1:AP000471 | 72466 | AP000471 | Homo sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | INHomo sapiens | 36,875 | 13-Sep-99 |
| rx00427 | 909 | GB_BA1:MSGY126 | 37164 | AD000012 | Mycobacterium tuberculosis sequence from clone y126. | Mycobacterium tuberculosis | 60,022 | 10-DEC-1996 |
| | | GB_BA1:MTY13D12 | 37085 | Z80343 | Mycobacterium tuberculosis H37Rv complete genome; segment 156/162. | Mycobacterium tuberculosis | 60,022 | 17-Jun-98 |
| | | GB_HTG1:CEY48C3 | 270193 | Z92855 | Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Caenorhabditis elegans | 28,013 | 29-MAY-1999 |
| rx00483 | 1587 | GB_PR2:HSAF001550 | 173882 | AF001550 | Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence. | Homo sapiens | 38,226 | 22-Aug-97 |
| | | GB_BA1:LLCPJW565 | 12828 | Y12736 | Lactococcus lactis cremoris plasmid pJW565 DNA, abliM, abliR genes and oriX. | Lactococcus lactis subsp. cremoris | 37,492 | 01-MAR-1999 |
| | | GB_HTG2:AC006754 | 206217 | AC006754 | Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***; 5 unordered pieces. | Caenorhabditis elegans | 36,648 | 23-Feb-99 |
| rx00511 | 615 | GB_PR3:HSE127C11 | 38423 | Z74581 | Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS. | Homo sapiens | 39,831 | 23-Nov-99 |
| | | GB_PR3:HSE127C11 | 38423 | Z74581 | Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS. | Homo sapiens | 36,409 | 23-Nov-99 |
| rx00512 | 718 | GB_BA1:MTCY22G8 | 22550 | Z95585 | Mycobacterium tuberculosis H37Rv complete genome; segment 49/162. | Mycobacterium tuberculosis | 56,232 | 17-Jun-98 |
| | | GB_BA1:MSGLTA | 1776 | X60513 | M.smegmatis gltA gene for citrate synthase. | Mycobacterium smegmatis | 56,143 | 20-Sep-91 |
| | | GB_BA2:ECU73857 | 128824 | U73857 | Escherichia coli chromosome minutes 6-8. | Escherichia coli | 48,563 | 14-Jul-99 |
| rx00517 | 1164 | GB_HTG2:AC006911 | 298804 | AC006911 | Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***; 15 unordered pieces. | Caenorhabditis elegans | 37,889 | 24-Feb-99 |
| | | GB_HTG2:AC006911 | 298804 | AC006911 | Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***; 15 unordered pieces. | Caenorhabditis elegans | 37,889 | 24-Feb-99 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|---|--------------------------------------|--------|-------------|
| rx00518 | 320 | GB_EST29:AI602158 | 481 | AI602158 | UI-R-AB0-vy-a-01-0-UI.s2 UI-R-AB0 Rattus norvegicus cDNA clone UI-R-AB0-vy-a-01-0-UI 3', mRNA sequence. | Rattus norvegicus | 40,833 | 21-Apr-99 |
| | | GB_BA2:ECU73857 | 128824 | U73857 | Escherichia coli chromosome minutes 6-8. | Escherichia coli | 49,688 | 14-Jul-99 |
| | | GB_BA2:STU51879 | 8371 | U51879 | Salmonella typhimurium propionate catabolism operon: RpoN activator protein homolog (prpR), carboxyphosphoenolpyruvate phosphonmutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds. | Salmonella typhimurium | 50,313 | 5-Aug-99 |
| rx00606 | 2378 | GB_BA2:AE000140 | 12498 | AE000140 | Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome. | Escherichia coli | 49,688 | 12-Nov-98 |
| | | GB_EST32:AU068253 | 376 | AU068253 | AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence. | Oryza sativa | 41,333 | 7-Jun-99 |
| | | GB_EST13:AA363046 | 329 | AA363046 | EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence. | Homo sapiens | 34,347 | 21-Apr-97 |
| | | GB_EST32:AU068253 | 376 | AU068253 | AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence. | Oryza sativa | 41,899 | 7-Jun-99 |
| rx00635 | 1860 | GB_BA1:PAORF1 | 1440 | X13378 | Pseudomonas amyloclavata DNA for ORF 1. | Pseudomonas amyloclavata | 53,912 | 14-Jul-95 |
| | | GB_BA1:PAORF1 | 1440 | X13378 | Pseudomonas amyloclavata DNA for ORF 1. | Pseudomonas amyloclavata | 54,422 | 14-Jul-95 |
| rx00679 | 1389 | GB_PL2:AC010871 | 80381 | AC010871 | Arabidopsis thaliana chromosome III BAC T16011 genomic sequence, complete sequence. | Arabidopsis thaliana | 38,244 | 13-Nov-99 |
| | | GB_PL1:AT81KBGEN | 81493 | X98130 | A.thaliana 81kb genomic sequence. | Arabidopsis thaliana | 36,091 | 12-MAR-1997 |
| | | GB_PL2:AC010871 | 80381 | AC010871 | Arabidopsis thaliana chromosome III BAC T16011 genomic sequence, complete sequence. | Arabidopsis thaliana | 37,135 | 13-Nov-99 |
| rx00680 | 441 | GB_PR3:AC004058 | 38400 | AC004058 | Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence. | Homo sapiens | 36,165 | 30-Sep-98 |
| | | GB_PL1:AT81KBGEN | 81493 | X98130 | A.thaliana 81kb genomic sequence. | Arabidopsis thaliana | 38,732 | 12-MAR-1997 |
| | | GB_PL1:AB026648 | 43481 | AB026648 | Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence. | Arabidopsis thaliana | 38,732 | 07-MAY-1999 |
| rx00682 | 2022 | GB_HTG3:AC010325 | 197110 | AC010325 | Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***. 40 unordered pieces. | Homo sapiens | 37,976 | 15-Sep-99 |
| | | GB_HTG3:AC010325 | 197110 | AC010325 | Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***. 40 unordered pieces. | Homo sapiens | 37,976 | 15-Sep-99 |
| rx00683 | 1215 | GB_PR4:AC008179 | 181745 | AC008179 | Homo sapiens clone NH0576F01, complete sequence. | Homo sapiens | 37,143 | 28-Sep-99 |
| | | GB_BA2:AE000896 | 10707 | AE000896 | Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome. | Methanobacterium thermoautotrophicum | 38,429 | 15-Nov-97 |
| | | GB_IN1:DMBR7A4 | 212734 | AL109630 | Drosophila melanogaster clone BACR7A4. | Drosophila melanogaster | 36,454 | 30-Jul-99 |
| | | GB_EST35:AV163010 | 273 | AV163010 | AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA cloneMus musculus 3110006J22, mRNA sequence. | Mus musculus | 41,758 | 8-Jul-99 |
| rx00686 | 927 | GB_HTG2:HSDJ137K2 | 190223 | AL049820 | Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***. in unordered pieces. | Homo sapiens | 38,031 | 03-DEC-1999 |
| | | GB_HTG2:HSDJ137K2 | 190223 | AL049820 | Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING IN PROGRESS ***. in unordered pieces. | Homo sapiens | 38,031 | 03-DEC-1999 |
| | | GB_EST12:AA284399 | 431 | AA284399 | zs57b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5', mRNA sequence. | Homo sapiens | 39,205 | 14-Aug-97 |
| rx00700 | 927 | GB_EST34:AI785570 | 454 | AI785570 | uj44403.x1 Sugano mouse liver milia Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence. | Mus musculus | 41,943 | 2-Jul-99 |

TABLE 4: ALIGNMENT RESULTS

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|-------------------|--------|----------|--|-------------------------------|--------|-------------|
| GB_EST25:AI256147 | 684 | AI256147 | ui95e12.x1 Sugano mouse liver milia Mus musculus cDNA clone IMAGE:1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence. | Mus musculus | 40,791 | 12-Nov-98 |
| GB_BA1:CARCG12 | 2079 | X14979 | C. aurantiacus reaction center genes 1 and 2. | Chloroflexus aurantiacus | 37,721 | 23-Apr-91 |
| GB_BA1:SC7H2 | 42655 | AL109732 | Streptomyces coelicolor cosmid 7H2. | Streptomyces coelicolor A3(2) | 56,646 | 2-Aug-99 |
| GB_BA1:MTCY274 | 39991 | Z74024 | Mycobacterium tuberculosis H37Rv complete genome; segment 126/162. | Mycobacterium tuberculosis | 37,369 | 19-Jun-98 |
| GB_BA2:REU60056 | 2520 | U60056 | Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds. | Ralstonia eutropha | 51,087 | 16-OCT-1998 |
| GB_GSS15:AQ604477 | 505 | AQ604477 | HS_2116_B1_G07_MR C1T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence. | Homo sapiens | 39,617 | 10-Jun-99 |
| GB_EST11:AA224340 | 443 | AA224340 | zr14e07.s1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence. | Homo sapiens | 35,129 | 11-MAR-1998 |
| GB_EST5:N30648 | 291 | N30648 | yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone Homo sapiens IMAGE:258219 3', mRNA sequence. | Homo sapiens | 43,986 | 5-Jan-96 |
| GB_BA1:MTCY10D7 | 39800 | Z79700 | Mycobacterium tuberculosis H37Rv complete genome; segment 44/162. | Mycobacterium tuberculosis | 63,327 | 17-Jun-98 |
| GB_BA1:MLCL373 | 37304 | AL035500 | Mycobacterium leprae cosmid L373. | Mycobacterium leprae | 62,300 | 27-Aug-99 |
| GB_BA2:AF128399 | 2842 | AF128399 | Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinylPseudomonas aeruginosa CoA synthetase alpha subunit (sucD) genes, complete cds. | Pseudomonas aeruginosa | 53,698 | 25-MAR-1999 |
| GB_HTG2:AC008158 | 118792 | AC008158 | Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN Homo sapiens PROGRESS ***, 14 unordered pieces. | Homo sapiens | 35,135 | 28-Jul-99 |
| GB_HTG2:AC008158 | 118792 | AC008158 | Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN Homo sapiens PROGRESS ***, 14 unordered pieces. | Homo sapiens | 35,135 | 28-Jul-99 |
| GB_PR3:AC005017 | 137176 | AC005017 | Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence. | Homo sapiens | 35,864 | 8-Aug-98 |
| GB_BA1:MTV017 | 67200 | AL021897 | Mycobacterium tuberculosis H37Rv complete genome; segment 48/162. | Mycobacterium tuberculosis | 40,331 | 24-Jun-99 |
| GB_BA1:MLCB1222 | 34714 | AL049491 | Mycobacterium leprae cosmid B1222. | Mycobacterium leprae | 61,170 | 27-Aug-99 |
| GB_PR2:HS151B14 | 128942 | Z82188 | Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene.pseudogene similar to ribosomal protein L39,RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence. | Homo sapiens | 37,455 | 16-Jun-99 |
| GB_PL2:AF016327 | 616 | AF016327 | Hordeum vulgare Barpermi1 (perm1) mRNA, partial cds. | Hordeum vulgare | 41,311 | 01-OCT-1997 |
| GB_HTG2:HSDJ319M7 | 128208 | AL079341 | Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING Homo sapiens IN PROGRESS ***, in unordered pieces. | Homo sapiens | 36,845 | 30-Nov-99 |
| GB_HTG2:HSDJ319M7 | 128208 | AL079341 | Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING Homo sapiens IN PROGRESS ***, in unordered pieces. | Homo sapiens | 36,845 | 30-Nov-99 |
| GB_BA1:MTV022 | 13025 | AL021925 | Mycobacterium tuberculosis H37Rv complete genome; segment 100/162. | Mycobacterium tuberculosis | 63,101 | 17-Jun-98 |
| GB_BA1:AB019513 | 4417 | AB019513 | Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds. | Streptomyces coelicolor | 41,312 | 13-Nov-98 |
| GB_PL1:SCSFAARP | 7008 | X68020 | S.cerevisiae SFA and ARP genes. | Saccharomyces cerevisiae | 36,288 | 29-Nov-94 |
| GB_BA1:MTY15C10 | 33050 | Z95436 | Mycobacterium tuberculosis H37Rv complete genome; segment 154/162. | Mycobacterium tuberculosis | 39,980 | 17-Jun-98 |
| GB_BA1:MLCB2548 | 38916 | AL023093 | Mycobacterium leprae cosmid B2548. | Mycobacterium leprae | 39,435 | 27-Aug-99 |
| GB_BA2:AF169031 | 1141 | AF169031 | Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds. | Xanthomonas oryzae pv. oryzae | 46,232 | 14-Sep-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|----------------------------|--------|-------------|
| rx00872 | 1077 | GB_IN1:CEF23H12 | 35564 | Z74472 | Caenorhabditis elegans cosmid F23H12, complete sequence. | Caenorhabditis elegans | 34,502 | 08-OCT-1999 |
| | | GB_HTG2:AC007263 | 167390 | AC007263 | Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN | Homo sapiens | 35,714 | 24-MAY-1999 |
| | | | | | PROGRESS ***, 5 ordered pieces. | | | |
| | | GB_HTG2:AC007263 | 167390 | AC007263 | Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN | Homo sapiens | 35,714 | 24-MAY-1999 |
| | | | | | PROGRESS ***, 5 ordered pieces. | | | |
| rx00879 | 2241 | GB_BA1:MTV049 | 40360 | AL022021 | Mycobacterium tuberculosis H37Rv complete genome; segment 81/162. | Mycobacterium tuberculosis | 36,981 | 19-Jun-98 |
| | | GB_PL2:CDU236897 | 1827 | AJ236897 | Candida dubliniensis ACT1 gene, exons 1-2. | Candida dubliniensis | 38,716 | 1-Sep-99 |
| | | GB_PL1:CAACT1A | 3206 | X16377 | Candida albicans act1 gene for actin. | Candida albicans | 36,610 | 10-Apr-93 |
| rx00909 | 955 | GB_BA2:AF010496 | 189370 | AF010496 | Rhodobacter capsulatus strain SB1003, partial genome. | Rhodobacter capsulatus | 51,586 | 12-MAY-1998 |
| | | GB_BA1:RMPHA | 7888 | X93358 | Rhizobium meliloti pha[A,B,C,D,E,F,G] genes. | Sinorhizobium meliloti | 48,367 | 12-MAR-1999 |
| | | GB_EST16:C23528 | 317 | C23528 | C23528 Japanese flounder spleen Paralicthys olivaceus cDNA clone HB5(2), mRNA sequence. | Paralicthys olivaceus | 41,640 | 28-Sep-99 |
| rx00913 | 2118 | GB_HTG2:AC007734 | 188267 | AC007734 | Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN | Homo sapiens | 34,457 | 5-Jun-98 |
| | | | | | PROGRESS ***, 18 unordered pieces. | | | |
| | | GB_HTG2:AC007734 | 188267 | AC007734 | Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN | Homo sapiens | 34,457 | 5-Jun-98 |
| | | | | | PROGRESS ***, 18 unordered pieces. | | | |
| | | GB_EST18:AA709478 | 406 | AA709478 | w34a05.r1 Siratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:1224272 5', mRNA sequence. | Mus musculus | 42,065 | 24-DEC-1997 |
| rx00945 | 1095 | GB_HTG4:AC010351 | 220710 | AC010351 | Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN | Homo sapiens | 36,448 | 31-OCT-1999 |
| | | | | | PROGRESS ***, 68 unordered pieces. | | | |
| | | GB_HTG4:AC010351 | 220710 | AC010351 | Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN | Homo sapiens | 36,448 | 31-OCT-1999 |
| | | | | | PROGRESS ***, 68 unordered pieces. | | | |
| | | GB_BA1:MTCY05A6 | 38631 | Z96072 | Mycobacterium tuberculosis H37Rv complete genome; segment 120/162. | Mycobacterium tuberculosis | 36,218 | 17-Jun-98 |
| rx00965 | | | | | | | | |
| rx00999 | 1575 | GB_PAT:E13660 | 1916 | E13660 | gDNA encoding 6-phosphogluconate dehydrogenase. | Corynebacterium glutamicum | 98,349 | 24-Jun-98 |
| | | GB_BA1:MTCY359 | 36021 | Z83859 | Mycobacterium tuberculosis H37Rv complete genome; segment 84/162. | Mycobacterium tuberculosis | 38,520 | 17-Jun-98 |
| | | GB_BA1:MLCB1788 | 39228 | AL008609 | Mycobacterium leprae cosmid B1788. | Mycobacterium leprae | 64,355 | 27-Aug-99 |
| rx01015 | 442 | GB_BA1:MTV008 | 63033 | AL021246 | Mycobacterium tuberculosis H37Rv complete genome; segment 108/162. | Mycobacterium tuberculosis | 39,860 | 17-Jun-98 |
| | | GB_BA1:MTV008 | 63033 | AL021246 | Mycobacterium tuberculosis H37Rv complete genome; segment 108/162. | Mycobacterium tuberculosis | 39,120 | 17-Jun-98 |
| rx01025 | 1119 | GB_BA1:SC7A1 | 32039 | AL034447 | Streptomyces coelicolor cosmid 7A1. | Streptomyces coelicolor | 55,287 | 15-DEC-1998 |
| | | GB_BA1:MSGB1723CS | 38477 | L78825 | Mycobacterium leprae cosmid B1723 DNA sequence. | Mycobacterium leprae | 56,847 | 15-Jun-96 |
| | | GB_BA1:MLCB637 | 44882 | Z99263 | Mycobacterium leprae cosmid B637. | Mycobacterium leprae | 56,676 | 17-Sep-97 |
| rx01048 | 1347 | GB_BA2:AF017444 | 3067 | AF017444 | Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds. | Sinorhizobium meliloti | 53,660 | 2-Nov-97 |
| rx01049 | 1605 | GB_BA1:BSUB0013 | 218470 | Z99116 | Bacillus subtilis complete genome (section 13 of 21); from 2395261 to 2613730. | Bacillus subtilis | 37,255 | 26-Nov-97 |
| | | GB_VI:HSV2HG52 | 154746 | Z86099 | Herpes simplex virus type 2 (strain HG52), complete genome. | human herpesvirus 2 | 38,081 | 04-DEC-1998 |
| | | GB_HTG2:AC002518 | 131855 | AC002518 | Homo sapiens chromosome X clone BWXD20, *** SEQUENCING IN PROGRESS | Homo sapiens | 35,647 | 2-Sep-97 |
| | | | | | ***, 11 unordered pieces. | | | |
| | | GB_HTG2:AC002518 | 131855 | AC002518 | Homo sapiens chromosome X clone BWXD20, *** SEQUENCING IN PROGRESS | Homo sapiens | 35,647 | 2-Sep-97 |
| | | | | | ***, 11 unordered pieces. | | | |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|------------------------------|---------|--------------------------------------|
| rx01077 | 1494 | GB_HTG2:AC002518 | 131855 | AC002518 | Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces. | Homo sapiens | 26,180 | 2-Sep-97 |
| | | GB_PR3:HSDJ653C5 | 85237 | AL049743 | Human DNA sequence from clone 653C5 on chromosome 1p21.3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence. | Homo sapiens | 36,462 | 23-Nov-99 |
| | | GB_BA1:ECU29579 | 72221 | U29579 | Escherichia coli K-12 genome; approximately 61 to 62 minutes. | Escherichia coli | 41,808 | 1-Jul-95 |
| | | GB_BA1:ECU29579 | 72221 | U29579 | Escherichia coli K-12 genome; approximately 61 to 62 minutes. | Escherichia coli | 36,130 | 1-Jul-95 |
| rx01089 | 873 | GB_GSS8:AQ044021 | 387 | AQ044021 | CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence. | Homo sapiens | 36,528 | 14-Jul-98 |
| | | GB_GSS8:AQ042907 | 392 | AQ042907 | CIT-HSP-2318D17.TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence. | Homo sapiens | 35,969 | 14-Jul-98 |
| | | GB_GSS8:AQ044021 | 387 | AQ044021 | CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence. | Homo sapiens | 44,545 | 14-Jul-98 |
| rx01093 | 1554 | GB_BA1:CORPYK1 | 2795 | L27126 | Corynebacterium pyruvate kinase gene, complete cds. | Corynebacterium glutamicum | 100,000 | 07-DEC-1994 |
| | | GB_BA1:MTCY01B2 | 35938 | Z95554 | Mycobacterium tuberculosis H37Rv complete genome; segment 72/162. | Mycobacterium tuberculosis | 83,771 | 17-Jun-98 |
| | | GB_BA1:MIJ65430 | 1439 | U65430 | Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds. | Mycobacterium intracellulare | 67,061 | 23-DEC-1996 |
| rx01099 | 948 | GB_BA2:AF045998 | 780 | AF045998 | Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds. | Corynebacterium glutamicum | 99,615 | 19-Feb-98 |
| | | GB_BA2:AF051846 | 738 | AF051846 | Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds. | Corynebacterium glutamicum | 100,000 | 12-MAR-1998 |
| rx01111 | 541 | GB_GSS1:FR0005503 | 619 | Z89313 | F.rubripes GSS sequence, clone 079B16aE8, genomic survey sequence. | Fugu rubripes | 37,785 | 01-MAR-1997 |
| | | GB_PR3:AC004083 | 177014 | AC004063 | Homo sapiens chromosome 4 clone B32l8, complete sequence. | Homo sapiens | 35,835 | 10-Jul-98 |
| | | GB_PR3:HS1178121 | 62268 | AL109852 | Human DNA sequence from clone RP5-1178121 on chromosome X, complete sequence. | Homo sapiens | 37,873 | 01-DEC-1999 |
| | | GB_HTG3:AC009301 | 163369 | AC009301 | Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces. | Homo sapiens | 37,240 | 13-Aug-99 |
| rx01130 | 687 | GB_HTG3:AC009444 | 164587 | AC009444 | Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces. | Homo sapiens | 38,416 | 22-Aug-99 |
| | | GB_HTG3:AC009444 | 164587 | AC009444 | Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces. | Homo sapiens | 38,416 | 22-Aug-99 |
| rx01193 | 1572 | GB_IN1:DMC66A1 | 34127 | AL031227 | Drosophila melanogaster cosmid 66A1. | Drosophila melanogaster | 38,416 | 05-OCT-1998 |
| | | GB_BA1:CGASO19 | 1452 | X76875 | C.glutamicum (ASO 19) ATPase beta-subunit gene. | Corynebacterium glutamicum | 99,931 | 27-OCT-1994 |
| | | EM_PAT:E09634 | 1452 | E09634 | Brevibacterium flavum UncD gene whose gene product is involved in | Corynebacterium glutamicum | 99,242 | 07-OCT-1997 (Rel. 52, Created) |
| rx01194 | 495 | GB_BA1:MLU15186 | 36241 | U15186 | Mycobacterium leprae cosmid L471. | Mycobacterium leprae | 39,153 | 09-MAR-1995 |
| | | EM_PAT:E09634 | 1452 | E09634 | Brevibacterium flavum UncD gene whose gene product is involved in | Corynebacterium glutamicum | 100,000 | 07-OCT-1997 (Rel. 52, Created) |
| | | GB_BA1:CGASO19 | 1452 | X76875 | C.glutamicum (ASO 19) ATPase beta-subunit gene. | Corynebacterium glutamicum | 100,000 | 27-OCT-1994 |
| rx01200 | | GB_VI:HEPCRE4B | 414 | X60570 | Hepatitis C genomic RNA for putative envelope protein (RE4B isolate). | Hepatitis C virus | 36,769 | 5-Apr-92 |
| rx01201 | 1764 | GB_BA1:SLATPSYNA | 8560 | Z22806 | S.lividans i protein and ATP synthase genes. | Streptomyces lividans | 66,269 | 01-MAY-1995 |
| | | GB_BA1:MTCY373 | 35516 | Z73419 | Mycobacterium tuberculosis H37Rv complete genome; segment 57/162. | Mycobacterium tuberculosis | 65,437 | 17-Jun-98 |

TABLE 4: ALIGNMENT RESULTS

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|-------------------|--------|----------|--|--------|-------------|
| GB_BA2:ECU78086 | 4759 | U78086 | Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and Escherichia coli O-chain length regulator (wzz) genes, complete cds. | 59,735 | 5-Nov-97 |
| GB_BA1:D90841 | 20226 | D90841 | E. coli genomic DNA, Kohara clone #351(45.1-45.5 min.). | 37,904 | 21-MAR-1997 |
| GB_PR3:AC004103 | 144368 | AC004103 | Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence. | 37,340 | 18-Apr-98 |
| GB_HTG3:AC007383 | 215529 | AC007383 | Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces. | 36,385 | 25-Sep-99 |
| GB_HTG3:AC007383 | 215529 | AC007383 | Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces. | 36,385 | 25-Sep-99 |
| GB_BA2:AE000487 | 13889 | AE000487 | Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome. | 39,494 | 12-Nov-98 |
| GB_BA1:MTV016 | 53662 | AL021841 | Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. | 46,252 | 23-Jun-99 |
| GB_BA1:U00022 | 36411 | U00022 | Mycobacterium leprae cosmid L308. | 46,368 | 01-MAR-1994 |
| GB_HTG4:AC009245 | 215767 | AC009245 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces. | 36,016 | 2-Nov-99 |
| GB_HTG4:AC009245 | 215767 | AC009245 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces. | 36,016 | 2-Nov-99 |
| GB_HTG4:AC009245 | 215767 | AC009245 | Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces. | 39,618 | 2-Nov-99 |
| GB_HTG6:AC007186 | 225851 | AC007186 | Drosophila melanogaster chromosome 2 clone BACR03D08 (D569) RPCI-98 03.D.6 Drosophila melanogaster map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 91 unordered pieces. | 35,366 | 07-DEC-1999 |
| GB_HTG6:AC007147 | 202291 | AC007147 | Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPCI-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces. | 35,366 | 07-DEC-1999 |
| GB_HTG3:AC010207 | 207890 | AC010207 | Homo sapiens clone RPCI11-375120, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces. | 34,821 | 16-Sep-99 |
| GB_BA2:AF109682 | 990 | AF109682 | Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds. | 58,487 | 19-OCT-1999 |
| GB_HTG2:AC006759 | 103725 | AC006759 | Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces. | 37,963 | 25-Feb-99 |
| GB_HTG2:AC006759 | 103725 | AC006759 | Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces. | 37,963 | 25-Feb-99 |
| GB_BA1:MTY20B11 | 36330 | Z95121 | Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. | 38,011 | 17-Jun-98 |
| GB_BA1:XANXANAB | 3410 | M83231 | Xanthomonas campestris phosphoglucosylase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds. | 47,726 | 26-Apr-93 |
| GB_GSS10:AQ194038 | 697 | AQ194038 | RPCI11-47D24. T.J RPCI-11 Homo sapiens genomic clone RPCI-11-47D24, genomic survey sequence. | 36,599 | 20-Apr-99 |
| GB_BA1:MTY20B11 | 36330 | Z95121 | Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. | 36,940 | 17-Jun-98 |
| GB_GSS3:B10037 | 974 | B10037 | T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence. | 35,284 | 14-MAY-1997 |
| GB_GSS3:B09549 | 1097 | B09549 | T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence. | 38,324 | 14-MAY-1997 |
| GB_BA1:MTCY71 | 42729 | Z92771 | Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. | 39,778 | 10-Feb-98 |
| GB_HTG5:AC007547 | 262181 | AC007547 | Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces. | 32,658 | 16-Nov-99 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|---|-------------------------------|---------|-------------|
| rx01392 | 1200 | GB_HTG5:AC007547 | 262181 | AC007547 | Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces. | Homo sapiens | 38,395 | 16-Nov-99 |
| | | GB_BA2:AF072709 | 8366 | AF072709 | Streptomyces lividans amplifiable element AUD4; putative regulator, putative ferredoxin, putative cytochrome P450 oxidoreductase, and putative oxidoreductase genes, complete cds; and unknown genes. | Streptomyces lividans | 55,221 | 8-Jul-98 |
| | | GB_BA1:CGLYSEG | 2374 | X96471 | C-glutamicum lysE and lysG genes. | Corynebacterium glutamicum | 100,000 | 24-Feb-97 |
| | | GB_PR4:AC005906 | 185952 | AC005906 | Homo sapiens 12p13.3 BAC RPC11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence. | Homo sapiens | 36,756 | 30-Jan-99 |
| rx01436 | 1314 | GB_BA1:CGPTAACKA | 3657 | X89084 | C-glutamicum pta gene and ackA gene. | Corynebacterium glutamicum | 100,000 | 23-MAR-1999 |
| | | GB_BA1:D90861 | 14839 | D90861 | E. coli genomic DNA, Kohara clone #405(52.0-52.3 min.). | Escherichia coli | 53,041 | 29-MAY-1997 |
| | | GB_PAT:E02087 | 1200 | E02087 | DNA encoding acetate kinase protein form Escherichia coli. | Escherichia coli | 54,461 | 29-Sep-97 |
| rx01468 | 948 | GB_GSS1:HPU0627 | 280 | U60627 | Helicobacter pylori feoB-like DNA sequence, genomic survey sequence. | Helicobacter pylori | 39,286 | 9-Apr-97 |
| | | GB_EST31:AI701691 | 349 | AI701691 | we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence. | Homo sapiens | 39,412 | 3-Jun-99 |
| | | GB_EST15:AA480256 | 389 | AA480256 | ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975 3' similar to Homo sapiens gb:L19686_ma1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence. | Homo sapiens | 39,574 | 14-Aug-97 |
| rx01478 | 1959 | GB_BA1:SCI51 | 40745 | AL109848 | Streptomyces coelicolor cosmid I51. | Streptomyces coelicolor A3(2) | 54,141 | 16-Aug-99 |
| | | GB_BA1:SCE36 | 12581 | AL049763 | Streptomyces coelicolor cosmid E36. | Streptomyces coelicolor | 38,126 | 05-MAY-1999 |
| | | GB_BA1:CGU43535 | 2531 | U43535 | Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds. | Corynebacterium glutamicum | 41,852 | 9-Apr-97 |
| rx01482 | 1998 | GB_BA1:SC6G4 | 41055 | AL031317 | Streptomyces coelicolor cosmid 6G4. | Streptomyces coelicolor | 62,149 | 20-Aug-98 |
| | | GB_BA1:U00020 | 36947 | U00020 | Mycobacterium leprae cosmid B229. | Mycobacterium leprae | 38,303 | 01-MAR-1994 |
| rx01534 | | GB_BA1:MTCY77 | 22255 | Z95389 | Mycobacterium tuberculosis H37Rv complete genome; segment 146/162. | Mycobacterium tuberculosis | 38,179 | 18-Jun-98 |
| rx01535 | 1530 | GB_BA1:MLCB1222 | 34714 | AL049491 | Mycobacterium leprae cosmid B1222. | Mycobacterium leprae | 66,208 | 27-Aug-99 |
| | | GB_BA1:MTV017 | 67200 | AL021897 | Mycobacterium tuberculosis H37Rv complete genome; segment 48/162. | Mycobacterium tuberculosis | 38,553 | 24-Jun-99 |
| | | GB_BA1:PAU72494 | 4368 | U72494 | Pseudomonas aeruginosa fumA (fumC) and Mn superoxide dismutase (sodA) genes, complete cds. | Pseudomonas aeruginosa | 52,690 | 23-OCT-1996 |
| rx01550 | 1635 | GB_BA1:D90907 | 132419 | D90907 | Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885. | Synechocystis sp. | 56,487 | 7-Feb-99 |
| | | GB_IN2:AF073177 | 9534 | AF073177 | Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds. | Drosophila melanogaster | 55,100 | 1-Jul-99 |
| rx01562 | | GB_IN2:AF073179 | 3159 | AF073179 | Drosophila melanogaster glycogen phosphorylase (GlyP) mRNA, complete cds. | Drosophila melanogaster | 56,708 | 27-Apr-99 |
| rx01569 | 1482 | GB_BA1:D78182 | 7836 | D78182 | Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds. | Streptococcus mutans | 44,050 | 5-Feb-99 |
| | | GB_BA2:AF079139 | 4342 | AF079139 | Streptomyces venezuelae pikCD operon, complete sequence. | Streptomyces venezuelae | 38,587 | 28-OCT-1998 |
| | | GB_BA2:AF087022 | 1470 | AF087022 | Streptomyces venezuelae cytochrome P450 monooxygenase (pick) gene, complete cds. | Streptomyces venezuelae | 38,621 | 15-OCT-1998 |
| rx01570 | 978 | GB_BA1:MTCY63 | 38900 | Z96800 | Mycobacterium tuberculosis H37Rv complete genome; segment 16/162. | Mycobacterium tuberculosis | 59,035 | 17-Jun-98 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | |
|-------------------|--------|----------|--|---|---------|-------------|
| GB_BA2:AF097519 | 4594 | AF097519 | Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (mIB), glucose-1-phosphate thymidyl transferase (mIA), dTDP-4-keto-L-rhamnose reductase (mID), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (mIC), and rhamnosyl transferase (wbbL) genes, complete cds. | Klebsiella pneumoniae | 59,714 | 4-Nov-98 |
| GB_BA2:NGOCPSPS | 8905 | L09189 | Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphateNeisseria meningitidis thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene. | Neisseria meningitidis | 58,384 | 30-Jul-96 |
| GB_BA1:AB011413 | 12070 | AB011413 | Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds. | Streptomyces griseus | 57,500 | 7-Aug-98 |
| GB_BA1:AB011413 | 12070 | AB011413 | Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds. | Streptomyces griseus | 35,655 | 7-Aug-98 |
| GB_BA1:AB011413 | 12070 | AB011413 | Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds. | Streptomyces griseus | 57,843 | 7-Aug-98 |
| GB_BA1:AB011413 | 12070 | AB011413 | Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds. | Streptomyces griseus | 38,119 | 7-Aug-98 |
| GB_VI:CFU72240 | 4783 | U72240 | Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds. | Choristoneura fumiferana nucleopolyhedrovirus | 37,115 | 29-Jan-99 |
| GB_GSS10:AQ213248 | 408 | AQ213248 | HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence. | Homo sapiens | 34,559 | 18-Sep-98 |
| GB_GSS8:AQ070145 | 285 | AQ070145 | HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence. | Homo sapiens | 40,351 | 5-Aug-98 |
| GB_PR4:AF152510 | 2490 | AF152510 | Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds. | Homo sapiens | 34,298 | 14-Jul-99 |
| GB_PR4:AF152323 | 4605 | AF152323 | Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds. | Homo sapiens | 34,298 | 22-Jul-99 |
| GB_PR4:AF152509 | 2712 | AF152509 | Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence. | Homo sapiens | 34,298 | 14-Jul-99 |
| GB_HTG4:AC006590 | 127171 | AC006590 | Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces. | Drosophila melanogaster | 33,812 | 19-OCT-1999 |
| GB_HTG4:AC006590 | 127171 | AC006590 | Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces. | Drosophila melanogaster | 33,812 | 19-OCT-1999 |
| GB_GSS8:B99182 | 415 | B99182 | CIT-HSP-2280113.TR CIT-HSP Homo sapiens genomic clone 2280113, genomic survey sequence. | Homo sapiens | 36,111 | 26-Jun-98 |
| GB_BA1:BSUB0009 | 208780 | Z99112 | Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200. | Bacillus subtilis | 36,591 | 26-Nov-97 |
| GB_BA1:BSUB0009 | 208780 | Z99112 | Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200. | Bacillus subtilis | 34,941 | 26-Nov-97 |
| GB_HTG2:AC006247 | 174368 | AC006247 | Drosophila melanogaster chromosome 2 clone BACR48H10 (D505) RPCI-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 17 unordered pieces. | Drosophila melanogaster | 37,037 | 2-Aug-99 |
| GB_BA1:CGA224946 | 2408 | AJ224946 | Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase. | Corynebacterium glutamicum | 100,000 | 11-Aug-98 |
| GB_BA1:MTCY24A1 | 20270 | Z95207 | Mycobacterium tuberculosis H37Rv complete genome; segment 124/162. | Mycobacterium tuberculosis | 38,626 | 17-Jun-98 |
| GB_IN1:DMU15974 | 2994 | U15974 | Drosophila melanogaster kinesin-like protein (kip88d) mRNA, complete cds. | Drosophila melanogaster | 36,783 | 18-Jul-95 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|--|--|--------|-------------|
| rx01702 | 1155 | GB_BA1:CGFDA | 3371 | X17313 | Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13). | Corynebacterium glutamicum | 99,913 | 12-Sep-93 |
| | | GB_BA1:MTY13E10 | 35019 | Z95324 | Mycobacterium tuberculosis H37Rv complete genome; segment 18/162. | Mycobacterium tuberculosis | 38,786 | 17-Jun-98 |
| | | GB_BA1:MLCB4 | 36310 | AL023514 | Mycobacterium leprae cosmid B4. | Mycobacterium leprae | 38,238 | 27-Aug-99 |
| rx01743 | 901 | GB_IN2:CELC27H5 | 35840 | U14635 | Caenorhabditis elegans cosmid C27H5. | Caenorhabditis elegans | 35,334 | 13-Jul-95 |
| | | GB_EST24:AI167112 | 579 | AI167112 | xylem.est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence. | Populus balsamifera subsp. trichocarpa | 39,222 | 03-DEC-1998 |
| | | GB_GSS9:AQ102635 | 347 | AQ102635 | HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence. | Homo sapiens | 40,653 | 27-Aug-98 |
| rx01744 | 1662 | GB_BA1:MTCY01B2 | 35938 | Z95554 | Mycobacterium tuberculosis H37Rv complete genome; segment 72/162. | Mycobacterium tuberculosis | 36,650 | 17-Jun-98 |
| | | GB_GSS1:AF009226 | 665 | AF009226 | Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence. | Mycobacterium tuberculosis | 63,438 | 31-Jul-97 |
| | | GB_BA1:SCD78 | 36224 | AL034355 | Streptomyces coelicolor cosmid D78. | Streptomyces coelicolor | 53,088 | 26-Nov-98 |
| rx01745 | 836 | GB_BA1:MTCY190 | 34150 | Z70283 | Mycobacterium tuberculosis H37Rv complete genome; segment 98/162. | Mycobacterium tuberculosis | 62,081 | 17-Jun-98 |
| | | GB_BA1:MLCB22 | 40281 | Z98741 | Mycobacterium leprae cosmid B22. | Mycobacterium leprae | 61,364 | 22-Aug-97 |
| | | GB_BA2:AE000175 | 15067 | AE000175 | Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome. | Escherichia coli | 52,323 | 12-Nov-98 |
| rx01758 | 1140 | GB_PR3:H5S7G9 | 113872 | Z95116 | Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS. | Homo sapiens | 39,209 | 23-Nov-99 |
| | | GB_PL2:YSCH9866 | 39057 | U10397 | Saccharomyces cerevisiae chromosome VIII cosmid 9866. | Saccharomyces cerevisiae | 40,021 | 5-Sep-97 |
| | | GB_PL2:YSCH9986 | 41664 | U00027 | Saccharomyces cerevisiae chromosome VIII cosmid 9986. | Saccharomyces cerevisiae | 34,375 | 29-Aug-97 |
| rx01814 | 1785 | GB_BA1:ABCCCLB | 2058 | L24077 | Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds. | Acetobacter xylinus | 62,173 | 21-Sep-94 |
| | | GB_BA1:MTCY22D7 | 31859 | Z83866 | Mycobacterium tuberculosis H37Rv complete genome; segment 133/162. | Mycobacterium tuberculosis | 39,749 | 17-Jun-98 |
| | | GB_BA1:MTCY22D7 | 31859 | Z83866 | Mycobacterium tuberculosis H37Rv complete genome; segment 133/162. | Mycobacterium tuberculosis | 40,034 | 17-Jun-98 |
| rx01851 | 1809 | GB_GSS9:AQ142579 | 529 | AQ142579 | HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence. | Homo sapiens | 38,068 | 24-Sep-98 |
| | | GB_IN2:AC005889 | 108924 | AC005889 | Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1 clones DS06958 and DS03097, complete sequence. | Drosophila melanogaster | 36,557 | 30-OCT-1998 |
| | | GB_GSS1:AG008814 | 637 | AG008814 | Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence. | Homo sapiens | 35,316 | 7-Feb-99 |
| rx01859 | 1050 | GB_BA2:AF183408 | 63626 | AF183408 | Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds. | Microcystis aeruginosa | 36,364 | 03-OCT-1999 |
| | | GB_HTG5:AC008031 | 158889 | AC008031 | Trypanosoma brucei chromosome II clone RPCI93-25N14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces. | Trypanosoma brucei | 35,334 | 15-Nov-99 |
| | | GB_BA2:AF183408 | 63626 | AF183408 | Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds. | Microcystis aeruginosa | 36,529 | 03-OCT-1999 |
| rx01865 | 438 | GB_BA1:SERFDXA | 3869 | M61119 | Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds. | Saccharopolyspora erythraea | 59,862 | 13-MAR-1996 |
| | | GB_BA1:MTV005 | 37840 | AL010186 | Mycobacterium tuberculosis H37Rv complete genome; segment 51/162. | Mycobacterium tuberculosis | 61,949 | 17-Jun-98 |
| | | GB_BA1:MSGY348 | 40056 | AD000020 | Mycobacterium tuberculosis sequence from clone y348. | Mycobacterium tuberculosis | 59,908 | 10-DEC-1996 |
| rx01882 | 1113 | GB_PR1:HUMADRA2C | 1491 | J03853 | Human kidney alpha-2-adrenergic receptor mRNA, complete cds. | Homo sapiens | 36,899 | 27-Apr-93 |
| | | GB_PR4:HSU72648 | 4850 | U72648 | Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds. | Homo sapiens | 36,899 | 23-Nov-98 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|---|-------------------------------------|---------|-------------|
| rx01884 | 1913 | GB_GSS3:B42200 | 387 | B42200 | HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence. | Homo sapiens | 34,805 | 18-OCT-1997 |
| | | GB_BA1:MTCY48 | 35377 | Z74020 | Mycobacterium tuberculosis H37Rv complete genome; segment 69/162. | Mycobacterium tuberculosis | 37,892 | 17-Jun-98 |
| | | GB_BA1:SCO001206 | 9184 | AJ001206 | Streptomyces coelicolor A3(2), glycogen metabolism cluster II. | Streptomyces coelicolor | 40,413 | 29-MAR-1989 |
| | | GB_BA1:D90908 | 122349 | D90908 | Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234. | Synechocystis sp. | 47,792 | 7-Feb-99 |
| rx01886 | 897 | GB_GSS9:AQ116291 | 572 | AQ116291 | RPC111-49P6.TK.1 RPC1-11 Homo sapiens genomic clone RPC1-11-49P6, genomic survey sequence. | Homo sapiens | 43,231 | 20-Apr-99 |
| | | GB_BA2:AE001721 | 17632 | AE001721 | Thermotoga maritima section 33 of 136 of the complete genome. | Thermotoga maritima | 39,306 | 2-Jun-99 |
| | | GB_EST16:AA567090 | 596 | AA567090 | GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence. | Drosophila melanogaster | 42,807 | 28-Nov-98 |
| rx01887 | 1134 | GB_HTG6:AC008147 | 303147 | AC008147 | Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***; 102 unordered pieces. | Homo sapiens | 36,417 | 03-DEC-1999 |
| | | GB_HTG6:AC008147 | 303147 | AC008147 | Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***; 102 unordered pieces. | Homo sapiens | 37,667 | 03-DEC-1999 |
| | | GB_BA2:ALW243431 | 26953 | AJ243431 | Acinetobacter lwoffii wcz, wzb, wza, weeA, weeB, weeC, wzx, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1. | Acinetobacter lwoffii | 39,640 | 01-OCT-1999 |
| rx01888 | 658 | GB_HTG2:AC008197 | 125235 | AC008197 | Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPC1-98 02.L.12 Drosophila melanogaster map 94B-94C strain y; cn bw sp. *** SEQUENCING IN PROGRESS***; 113 unordered pieces. | Drosophila melanogaster | 32,969 | 2-Aug-99 |
| | | GB_HTG2:AC008197 | 125235 | AC008197 | Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPC1-98 02.L.12 Drosophila melanogaster map 94B-94C strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 113 unordered pieces. | Drosophila melanogaster | 32,969 | 2-Aug-99 |
| | | GB_EST36:A1881527 | 598 | A1881527 | 606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence. | Zea mays | 43,617 | 21-Jul-99 |
| rx01891 | 887 | GB_VI:HIV232971 | 621 | AJ232971 | Human immunodeficiency virus type 1 subtype C nef gene, patient MP83. | Human immunodeficiency virus type 1 | 40,040 | 05-MAR-1999 |
| | | GB_PL1:AFCHSE | 6158 | Y09542 | A.fumigatus chsE gene. | Aspergillus fumigatus | 37,844 | 1-Apr-87 |
| | | GB_PR3:AF064858 | 193387 | AF064858 | Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence. | Homo sapiens | 37,136 | 2-Jun-88 |
| rx01895 | 1051 | GB_BA1:CGL238250 | 1593 | AJ238250 | Corynebacterium glutamicum ndh gene. | Corynebacterium glutamicum | 100,000 | 24-Apr-99 |
| | | GB_BA2:AF038423 | 1376 | AF038423 | Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds. | Mycobacterium smegmatis | 65,254 | 05-MAY-1998 |
| | | GB_BA1:MTCY359 | 36021 | Z83859 | Mycobacterium tuberculosis H37Rv complete genome; segment 84/162. | Mycobacterium tuberculosis | 40,058 | 17-Jun-98 |
| rx01901 | 1383 | GB_BA1:MSGB38COS | 37114 | L01095 | M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds. | Mycobacterium leprae | 59,551 | 6-Sep-94 |
| | | GB_BA1:SCE63 | 37200 | AL035640 | Streptomyces coelicolor cosmid E63. | Streptomyces coelicolor | 39,468 | 17-MAR-1999 |
| | | GB_PR3:AF093117 | 147216 | AF093117 | Homo sapiens chromosome 7q10 BAC E3, complete sequence. | Homo sapiens | 39,291 | 02-OCT-1998 |
| rx01927 | 1503 | GB_BA1:CGPAN | 2164 | X95580 | C.glutamicum panB, panC & xylB genes. | Corynebacterium glutamicum | 38,384 | 11-MAY-1999 |
| | | GB_BA1:ASXYLA | 1905 | X59466 | Arthrobacter Sp. N.R.L. B3728 xylA gene for D-xylase(D-glucose) isomerase. | Arthrobacter sp. | 56,283 | 04-MAY-1992 |
| | | GB_HTG3:AC009500 | 176060 | AC009500 | Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***; 6 unordered pieces. | Homo sapiens | 37,593 | 24-Aug-99 |
| rx01952 | 1836 | GB_BA2:AE000739 | 13335 | AE000739 | Aquifex aeolicus section 71 of 109 of the complete genome. | Aquifex aeolicus | 36,309 | 25-MAR-1998 |
| | | GB_EST28:A1519629 | 612 | A1519629 | LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence. | Drosophila melanogaster | 41,941 | 16-MAR-1999 |
| | | GB_EST21:AA949396 | 767 | AA949396 | LD28277 5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence. | Drosophila melanogaster | 39,855 | 25-Nov-98 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|--|--------|-------------|
| rx01989 | 630 | GB_BA1:BSPGIA | 1822 | X16639 | Bacillus stearothermophilus pgjA gene for phosphoglucosyltransferase isoenzyme A (ECBacillus stearothermophilus 5.3.1.9). | 66,292 | 20-Apr-95 |
| | | GB_BA1:BSUB0017 | 217420 | Z99120 | Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420. | 37,255 | 26-Nov-97 |
| | | GB_BA2:AF132127 | 8452 | AF132127 | Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene. | 63,607 | 28-Sep-99 |
| rx02026 | 720 | GB_BA1:XSXCRBA | 3161 | X67744 | S.xylosus scrB and scrR genes. | 67,778 | 28-Nov-96 |
| | | GB_BA1:BSUB0020 | 212150 | Z99123 | Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550. | 35,574 | 26-Nov-97 |
| | | GB_BA1:BSGENR | 97015 | X73124 | B.subtilis genomic region (325 to 333). | 51,826 | 2-Nov-93 |
| rx02028 | 526 | GB_BA1:MTIC237 | 27030 | Z94752 | Mycobacterium tuberculosis H37Rv complete genome; segment 48/162. | 54,476 | 17-Jun-98 |
| | | GB_PL2:SCE9537 | 66030 | U18778 | Saccharomyces cerevisiae chromosome V cosmid 9537, 9581, 9495, 9867, and lambda clone 5898. | 36,100 | 1-Aug-97 |
| | | GB_GSS13:AQ501177 | 767 | AQ501177 | V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', genomic survey sequence. | 32,039 | 29-Apr-99 |
| rx02054 | 1140 | GB_BA1:MLCB1222 | 34714 | AL049491 | Mycobacterium leprae cosmid B1222. | 61,896 | 27-Aug-99 |
| | | GB_BA1:MTY13E12 | 43401 | Z95390 | Mycobacterium tuberculosis H37Rv complete genome; segment 147/162. | 59,964 | 17-Jun-98 |
| | | GB_BA1:MTU43540 | 3453 | U43540 | Mycobacterium tuberculosis rfaA, rhamnose biosynthesis protein (rfaA), and rmlC genes, complete cds. | 59,659 | 14-Aug-97 |
| rx02056 | 2891 | GB_PAT:E14601 | 4394 | E14601 | Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase. | 98,928 | 28-Jul-99 |
| | | GB_BA1:D84102 | 4394 | D84102 | Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds. | 98,928 | 6-Feb-99 |
| rx02061 | 1617 | GB_BA1:MTV006 | 22440 | AL021006 | Mycobacterium tuberculosis H37Rv complete genome; segment 54/162. | 39,265 | 18-Jun-98 |
| | | GB_HTG7:AC005883 | 211682 | AC005883 | Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces. | 37,453 | 08-DEC-1999 |
| | | GB_PL2:ATAC003033 | 84254 | AC003033 | Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence. | 37,711 | 19-DEC-1997 |
| | | GB_PL2:ATAC002334 | 75050 | AC002334 | Arabidopsis thaliana chromosome II BAC F25118 genomic sequence, complete sequence. | 37,711 | 04-MAR-1998 |
| rx02063 | 1350 | GB_BA1:SCGLGC | 1518 | X89733 | S.coelicolor DNA for glgC gene. | 56,972 | 12-Jul-99 |
| | | GB_GSS4:AQ687350 | 786 | AQ687350 | nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, Oryza sativa genomic survey sequence. | 40,696 | 1-Jul-99 |
| | | GB_EST38:AW028530 | 444 | AW028530 | wv27f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similarHomo sapiens to WP:TP3G11.6 CE04874.; mRNA sequence. | 36,795 | 27-OCT-1999 |
| rx02100 | 2348 | GB_BA1:MSGY151 | 37036 | AD000018 | Mycobacterium tuberculosis sequence from clone y151. | 40,156 | 10-DEC-1996 |
| | | GB_BA1:MTCY130 | 32514 | Z73902 | Mycobacterium tuberculosis H37Rv complete genome; segment 59/162. | 55,218 | 17-Jun-98 |
| | | GB_BA1:SCO001205 | 9589 | AJ001205 | Streptomyces coelicolor A3(2) glycogen metabolism cluster. | 38,475 | 29-MAR-1999 |
| rx02122 | 822 | GB_BA1:D90858 | 13548 | D90858 | E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.). | 38,586 | 29-MAY-1997 |
| | | GB_EST37:A1948595 | 469 | A1948595 | wq07d12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3', mRNA sequence. | 37,259 | 6-Sep-99 |
| | | GB_HTG3:AC010387 | 220665 | AC010387 | Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***, 77 unordered pieces. | 38,868 | 15-Sep-99 |
| rx02140 | 1200 | GB_BA1:MSGB1551CS | 36548 | L78813 | Mycobacterium leprae cosmid B1551 DNA sequence. | 51,399 | 15-Jun-96 |
| | | GB_BA1:MSGB1554CS | 36548 | L78814 | Mycobacterium leprae cosmid B1554 DNA sequence. | 51,399 | 15-Jun-96 |
| | | GB_RO:AF093099 | 2482 | AF093099 | Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds. | 36,683 | 01-OCT-1999 |
| rx02142 | 774 | GB_BA1:MTCY190 | 34150 | Z70283 | Mycobacterium tuberculosis H37Rv complete genome; segment 98/162. | 57,292 | 17-Jun-98 |
| | | GB_BA1:SC6G10 | 36734 | AL049497 | Streptomyces coelicolor cosmid 6G10. | 35,058 | 24-MAR-1999 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|--------------------|--------|----------|---|----------------------------|---------|-------------|
| rx02143 | 1011 | GB_BA1:AB016787 | 5550 | AB016787 | Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds. | Pseudomonas putida | 47,403 | 5-Aug-99 |
| | | GB_BA1:MTVCY190 | 34150 | Z70283 | Mycobacterium tuberculosis H37Rv complete genome; segment 98/162. | Mycobacterium tuberculosis | 57,317 | 17-Jun-98 |
| | | GB_BA1:MSGB1551CS | 36548 | L78813 | Mycobacterium leprae cosmid B1551 DNA sequence. | Mycobacterium leprae | 38,159 | 15-Jun-96 |
| | | GB_BA1:MSGB1554CS | 36548 | L78814 | Mycobacterium leprae cosmid B1554 DNA sequence. | Mycobacterium leprae | 38,159 | 15-Jun-96 |
| rx02144 | 1347 | GB_BA1:MTVCY190 | 34150 | Z70283 | Mycobacterium tuberculosis H37Rv complete genome; segment 98/162. | Mycobacterium tuberculosis | 55,530 | 17-Jun-98 |
| | | GB_HTG3:AC011500_0 | 300851 | AC011500 | Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***; 246 unordered pieces. | Homo sapiens | 39,659 | 18-Feb-00 |
| | | GB_HTG3:AC011500_0 | 300851 | AC011500 | Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***; 246 unordered pieces. | Homo sapiens | 39,659 | 18-Feb-00 |
| rx02147 | 1140 | GB_EST28:AI492095 | 485 | AI492095 | ig07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence. | Homo sapiens | 39,798 | 30-MAR-1999 |
| | | GB_EST10:AA157467 | 376 | AA157467 | zo50a01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence. | Homo sapiens | 36,436 | 11-DEC-1996 |
| | | GB_EST10:AA157467 | 376 | AA157467 | zo50a01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence. | Homo sapiens | 36,436 | 11-DEC-1996 |
| rx02149 | 1092 | GB_PR3:HSBK277P6 | 61698 | AL117347 | Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence. | Homo sapiens | 36,872 | 23-Nov-99 |
| | | GB_BA2:EMB065R075 | 360 | AF116423 | Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence. | Rhizobium etli | 43,175 | 06-DEC-1999 |
| | | GB_EST34:AI789323 | 574 | AI789323 | uk53g05.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1972760Mus musculus 5' similar to WP:K11H12.8 CE12160 ;. mRNA sequence. | Mus musculus | 39,715 | 2-Jul-99 |
| rx02175 | 1416 | GB_BA1:CGGLTG | 3013 | X66112 | C.glutamicum glt gene for citrate synthase and ORF. | Corynebacterium glutamicum | 100,000 | 17-Feb-95 |
| | | GB_BA1:MTVCY31 | 37630 | Z73101 | Mycobacterium tuberculosis H37Rv complete genome; segment 41/162. | Mycobacterium tuberculosis | 64,331 | 17-Jun-98 |
| | | GB_BA1:MLCB57 | 38029 | Z99494 | Mycobacterium leprae cosmid B57. | Mycobacterium leprae | 62,491 | 10-Feb-98 |
| rx02196 | 816 | GB_RO:RATDAPRP | 2819 | M76426 | Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds. | Rattus norvegicus | 38,791 | 31-MAY-1995 |
| | | GB_GSS8:AQ012162 | 763 | AQ012162 | 127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence. | Rhodobacter sphaeroides | 40,044 | 4-Jun-98 |
| | | GB_RO:RATDAPRP | 2819 | M76426 | Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds. | Rattus norvegicus | 37,312 | 31-MAY-1995 |
| rx02209 | 1694 | GB_BA1:AB025424 | 2995 | AB025424 | Corynebacterium glutamicum gene for aconitase, partial cds. | Corynebacterium glutamicum | 99,173 | 3-Apr-99 |
| | | GB_BA2:AF002133 | 15437 | AF002133 | Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds. | Mycobacterium avium | 40,219 | 26-MAR-1998 |
| rx02213 | 874 | GB_BA1:MTV007 | 32806 | AL021184 | Mycobacterium tuberculosis H37Rv complete genome; segment 64/162. | Mycobacterium tuberculosis | 38,253 | 17-Jun-98 |
| | | GB_BA1:AB025424 | 2995 | AB025424 | Corynebacterium glutamicum gene for aconitase, partial cds. | Corynebacterium glutamicum | 99,096 | 3-Apr-99 |
| | | GB_BA1:MTV007 | 32806 | AL021184 | Mycobacterium tuberculosis H37Rv complete genome; segment 64/162. | Mycobacterium tuberculosis | 34,937 | 17-Jun-98 |
| | | GB_BA2:AF002133 | 15437 | AF002133 | Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds. | Mycobacterium avium | 36,885 | 26-MAR-1998 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | |
|---------|------|-------------------|--------|----------|---|---------|-------------|
| rx02245 | 780 | GB_BA2:RCU23145 | 5960 | U23145 | Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-bisphosphatase-1,7-bisphosphatase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphatase carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon: pentose-5-phosphate-3-epimerase (cbbE), phosphoglycerate phosphatase (cbbZ), and cbbY genes, complete cds. | 48,701 | 28-OCT-1997 |
| | | GB_BA1:ECU82664 | 139818 | U82664 | Escherichia coli minutes 9 to 11 genomic sequence. | 39,119 | 11-Jan-97 |
| | | GB_HTG2:AC007922 | 158858 | AC007922 | Homo sapiens chromosome 18 clone hRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces. | 33,118 | 26-Jun-99 |
| rx02256 | 1125 | GB_BA1:CGGAPPGK | 3804 | X59403 | C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase. | 99,289 | 05-OCT-1992 |
| | | GB_BA1:SCC54 | 30753 | AL035591 | Streptomyces coelicolor cosmid C54. | 36,951 | 11-Jun-99 |
| | | GB_BA1:MTCY493 | 40790 | Z95844 | Mycobacterium tuberculosis H37Rv complete genome; segment 63/162. | 64,196 | 19-Jun-98 |
| rx02257 | 1338 | GB_BA1:CGGAPPGK | 3804 | X59403 | C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase. | 98,873 | 05-OCT-1992 |
| | | GB_BA1:MTCY493 | 40790 | Z95844 | Mycobacterium tuberculosis H37Rv complete genome; segment 63/162. | 61,273 | 19-Jun-98 |
| | | GB_BA2:MAU82749 | 2530 | U82749 | Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds. | 61,772 | 6-Jan-98 |
| rx02258 | 900 | GB_BA1:CGGAPPGK | 3804 | X59403 | C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase. | 99,667 | 05-OCT-1992 |
| | | GB_BA1:CORPEPC | 4885 | M25819 | C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds. | 100,000 | 15-DEC-1995 |
| | | GB_PAT:A09073 | 4885 | A09073 | C.glutamicum ppg gene for phosphoenol pyruvate carboxylase. | 100,000 | 25-Aug-93 |
| rx02259 | 2895 | GB_BA1:CORPEPC | 4885 | M25819 | C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds. | 100,000 | 15-DEC-1995 |
| | | GB_PAT:A09073 | 4885 | A09073 | C.glutamicum ppg gene for phosphoenol pyruvate carboxylase. | 100,000 | 25-Aug-93 |
| | | GB_BA1:CGPPC | 3292 | X14234 | Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31). | 99,827 | 12-Sep-93 |
| rx02288 | 969 | GB_PR3:HSDJ94E24 | 243145 | AL050317 | Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence. | 36,039 | 03-DEC-1999 |
| | | GB_HTG3:AC010091 | 159526 | AC010091 | Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces. | 35,331 | 11-Sep-99 |
| | | GB_HTG3:AC010091 | 159526 | AC010091 | Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces. | 35,331 | 11-Sep-99 |
| rx02292 | 798 | GB_BA2:AF125164 | 26443 | AF125164 | Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes. | 39,747 | 01-DEC-1999 |
| | | GB_GSS5:AAQ744695 | 827 | AQ744695 | HS_5505_A2_C06_SP6 RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence. | 39,185 | 16-Jul-99 |
| | | GB_EST14:AA381925 | 309 | AA381925 | EST95058 Activated T-cells I Homo sapiens cDNA 5' end, mRNA sequence. | 35,922 | 21-Apr-97 |
| rx02322 | 511 | GB_BA1:MTCY22G8 | 22550 | Z95585 | Mycobacterium tuberculosis H37Rv complete genome; segment 49/162. | 57,677 | 17-Jun-98 |
| | | GB_BA1:MTCY22G8 | 22550 | Z95585 | Mycobacterium tuberculosis H37Rv complete genome; segment 49/162. | 37,143 | 17-Jun-98 |
| rx02326 | 939 | GB_BA1:CGPYC | 3728 | Y09546 | Corynebacterium glutamicum pyc gene. | 100,000 | 08-MAY-1998 |
| | | GB_BA2:AF038548 | 3637 | AF038548 | Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds. | 100,000 | 24-DEC-1997 |
| | | GB_BA1:MTCY349 | 43523 | Z83018 | Mycobacterium tuberculosis H37Rv complete genome; segment 131/162. | 37,363 | 17-Jun-98 |
| rx02327 | 1083 | GB_BA1:CGPYC | 3728 | Y09548 | Corynebacterium glutamicum pyc gene. | 99,259 | 08-MAY-1998 |
| | | GB_BA2:AF038548 | 3637 | AF038548 | Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds. | 99,259 | 24-DEC-1997 |
| | | GB_BA1:MTCY349 | 43523 | Z83018 | Mycobacterium tuberculosis H37Rv complete genome; segment 131/162. | 41,317 | 17-Jun-98 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|--------------------------------|---------|-------------|
| rx02328 | 1719 | GB_BA1:CGPVC | 3728 | Y09548 | Corynebacterium glutamicum pyc gene. | Corynebacterium glutamicum | 100,000 | 08-MAY-1998 |
| | | GB_BA2:AF038548 | 3637 | AF038548 | Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds. | Corynebacterium glutamicum | 100,000 | 24-DEC-1997 |
| | | GB_PL2:AF097728 | 3916 | AF097728 | Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds. | Aspergillus terreus | 52,248 | 29-OCT-1998 |
| rx02332 | 1266 | GB_BA1:MSGLTA | 1776 | X60513 | M.smeigmatis gltA gene for citrate synthase. | Mycobacterium smegmatis | 58,460 | 20-Sep-91 |
| | | GB_BA2:ABU85944 | 1334 | U85944 | Antarctic bacterium DS2-3R citrate synthase (cisy) gene, complete cds. | Antarctic bacterium DS2-3R | 57,154 | 23-Sep-97 |
| | | GB_BA2:AE000175 | 15067 | AE000175 | Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome. | Escherichia coli | 38,164 | 12-Nov-88 |
| rx02333 | 1038 | GB_BA1:MSGLTA | 1776 | X60513 | M.smeigmatis gltA gene for citrate synthase. | Mycobacterium smegmatis | 58,928 | 20-Sep-91 |
| | | GB_PR4:HUAC002299 | 171681 | AC002299 | Homo sapiens Chromosome 16 BAC clone C1987-SKA-113A6 ~complete genomic | Homo sapiens | 33,070 | 23-Nov-99 |
| | | GB_HTG2:AC007889 | 127840 | AC007889 | sequence, complete sequence. | Drosophila melanogaster | 34,897 | 2-Aug-99 |
| | | | | | 48.E:12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces. | | | |
| rx02399 | 1467 | GB_BA1:CGACEA | 2427 | X75504 | C.glutamicum aceA gene and thix genes (partial). | Corynebacterium glutamicum | 100,000 | 9-Sep-94 |
| | | GB_BA1:CORACEA | 1905 | L28760 | Corynebacterium glutamicum isocitrate lyase (aceA) gene. | Corynebacterium glutamicum | 100,000 | 10-Feb-95 |
| | | GB_PAT:113693 | 2135 | 113693 | Sequence 3 from patent US 5439822. | Unknown. | 99,795 | 26-Sep-95 |
| rx02404 | 2340 | GB_BA1:CGACEB | 3024 | X78491 | C.glutamicum (ATCC 13032) aceB gene. | Corynebacterium glutamicum | 99,914 | 13-Jan-95 |
| | | GB_BA1:CORACEB | 2725 | L27123 | Corynebacterium glutamicum malate synthase (aceB) gene, complete cds. | Corynebacterium glutamicum | 99,786 | 8-Jun-95 |
| | | GB_BA1:PFEC2 | 5588 | Y11998 | P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open reading frames. | Pseudomonas fluorescens | 63,539 | 11-Jul-97 |
| rx02414 | 870 | GB_PR4:AC007102 | 176258 | AC007102 | Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence. | Homo sapiens | 35,069 | 2-Jun-99 |
| | | GB_HTG3:AC011214 | 183414 | AC011214 | Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING. | Homo sapiens | 36,885 | 03-OCT-1999 |
| | | GB_HTG3:AC011214 | 183414 | AC011214 | Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING. | Homo sapiens | 36,885 | 03-OCT-1999 |
| rx02435 | 681 | GB_BA2:AF101055 | 7457 | AF101055 | Clostridium acetobutylicum atp operon, complete sequence. | Clostridium acetobutylicum | 39,605 | 03-MAR-1999 |
| | | GB_OM:RABPKA | 4441 | J03247 | Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds. | Oryctolagus cuniculus | 36,061 | 27-Apr-93 |
| | | GB_OM:RABPLASISM | 4458 | M64656 | Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds. | Oryctolagus cuniculus | 36,000 | 22-Jun-98 |
| rx02440 | 963 | GB_EST14:AA417723 | 374 | AA417723 | zV01b12.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746207 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;, mRNA sequence. | Homo sapiens | 38,770 | 16-OCT-1997 |
| | | GB_EST11:AA215428 | 303 | AA215428 | zr95a07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:863412 3' similar to contains Alu repetitive element; mRNA sequence. | Homo sapiens | 39,934 | 13-Aug-97 |
| | | GB_BA1:MTCV77 | 22255 | Z95389 | Mycobacterium tuberculosis H37Rv complete genome; segment 146/162. | Mycobacterium tuberculosis | 38,889 | 18-Jun-98 |
| rx02453 | 876 | GB_EST14:AA426336 | 375 | AA426336 | zV53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3'; mRNA sequence. | Homo sapiens | 38,043 | 16-OCT-1997 |
| | | GB_BA1:STMAACC8 | 1353 | M55426 | S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds. | Streptomyces fradiae | 37,097 | 05-MAY-1993 |
| | | GB_PR3:AC004500 | 77538 | AC004500 | Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence. | Homo sapiens | 33,256 | 30-MAR-1998 |
| rx02474 | 897 | GB_BA1:AB009078 | 2686 | AB009078 | Brevibacterium saccharolyticum gene for L-2,3-butanediol dehydrogenase, complete cds. | Brevibacterium saccharolyticum | 96,990 | 13-Feb-99 |
| | | GB_OM:BTU71200 | 877 | U71200 | Bos taurus acetoin reductase mRNA, complete cds. | Bos taurus | 51,659 | 8-Oct-97 |
| | | GB_EST2:F12685 | 287 | F12685 | HSC3DA031 normalized Infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence | Homo sapiens | 41,508 | 14-Mar-95 |
| rx02480 | 1779 | GB_BA1:MTV012 | 70287 | AL021287 | Mycobacterium tuberculosis H37Rv complete genome; segment 132/162. | Mycobacterium tuberculosis | 36,737 | 23-Jun-99 |
| | | GB_BA1:SC6G10 | 36734 | AL049497 | Streptomyces coelicolor cosmid 6G10. | Streptomyces coelicolor | 35,511 | 24-MAR-1999 |
| rx02485 | | GB_BA1:AP000060 | 347800 | AP000060 | Aeropyrum pernix genomic DNA, section 3/7. | Aeropyrum pernix | 48,014 | 22-Jun-99 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|------------------------|--------|----------|---|----------------------------|--------|-------------|
| rx02492 | 840 | GB_BA1:STMPGM | 921 | M83661 | Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds. | Streptomyces coelicolor | 65,672 | 26-Apr-93 |
| | | GB_BA1:MTCY20G9 | 37218 | Z77162 | Mycobacterium tuberculosis H37Rv complete genome; segment 25/162. | Mycobacterium tuberculosis | 61,436 | 17-Jun-98 |
| | | GB_BA1:U00018 | 42991 | U00018 | Mycobacterium leprae cosmid B2168. | Mycobacterium leprae | 37,893 | 01-MAR-1994 |
| rx02528 | 1098 | GB_PR2:HS161N10 | 56075 | AL008707 | Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST. | Homo sapiens | 37,051 | 23-Nov-99 |
| | | GB_HTG2:AC008235 | 136017 | AC008235 | Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 | Drosophila melanogaster | 36,822 | 2-Aug-99 |
| | | | | | 15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 125 unordered pieces. | | | |
| | | GB_HTG2:AC008235 | 136017 | AC008235 | Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 | Drosophila melanogaster | 36,822 | 2-Aug-99 |
| | | | | | 15.B.19 map 94F-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 125 unordered pieces. | | | |
| rx02539 | 1641 | GB_BA2:RSU17129 | 17425 | U17129 | Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes. | Rhodococcus erythropolis | 66,117 | 16-Jul-99 |
| | | GB_BA1:MTV038 | 16094 | AL021933 | Mycobacterium tuberculosis H37Rv complete genome; segment 24/162. | Mycobacterium tuberculosis | 65,174 | 17-Jun-98 |
| | | GB_BA2:AF068264 | 3152 | AF068264 | Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds. | Pseudomonas aeruginosa | 65,448 | 18-MAR-1999 |
| rx02551 | 483 | GB_BA1:BACHYPTP | 17057 | D29985 | Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins. | Bacillus subtilis | 53,602 | 7-Feb-99 |
| | | GB_BA1:BACHUTWAPA28954 | | D31856 | Bacillus subtilis genome containing the hut and wapA loci. | Bacillus subtilis | 53,602 | 7-Feb-99 |
| | | GB_BA1:BSGBGLUC | 4290 | Z34526 | B. subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase. | Bacillus subtilis | 53,602 | 3-Jul-95 |
| rx02556 | 1281 | GB_HTG3:AC008128 | 335761 | AC008128 | Homo sapiens, *** SEQUENCING IN PROGRESS ***; 106 unordered pieces. | Homo sapiens | 34,022 | 22-Aug-99 |
| | | GB_HTG3:AC008128 | 335761 | AC008128 | Homo sapiens, *** SEQUENCING IN PROGRESS ***; 106 unordered pieces. | Homo sapiens | 34,022 | 22-Aug-99 |
| | | GB_PL2:AC005292 | 99053 | AC005292 | Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence. | Arabidopsis thaliana | 33,858 | 16-Apr-99 |
| rx02560 | 990 | GB_IN1:CEF07A11 | 35692 | Z66511 | Caenorhabditis elegans cosmid F07A11, complete sequence. | Caenorhabditis elegans | 36,420 | 2-Sep-99 |
| | | GB_EST32:AT731605 | 566 | AT731605 | BNLGH10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence. | Gossypium hirsutum | 38,095 | 11-Jun-99 |
| | | GB_IN1:CEF07A11 | 35692 | Z66511 | Caenorhabditis elegans cosmid F07A11, complete sequence. | Caenorhabditis elegans | 33,707 | 2-Sep-99 |
| rx02572 | 668 | GB_BA1:MTCY63 | 38900 | Z96800 | Mycobacterium tuberculosis H37Rv complete genome; segment 16/162. | Mycobacterium tuberculosis | 61,677 | 17-Jun-98 |
| | | GB_BA1:MTCY63 | 38900 | Z96800 | Mycobacterium tuberculosis H37Rv complete genome; segment 16/162. | Mycobacterium tuberculosis | 37,170 | 17-Jun-98 |
| | | GB_HTG1:HS24H01 | 46989 | AL121632 | Homo sapiens chromosome 21 clone LLNLC116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***; in unordered pieces. | Homo sapiens | 19,820 | 29-Sep-99 |
| rx02596 | 1326 | GB_BA1:MTV026 | 23740 | AL022076 | Mycobacterium tuberculosis H37Rv complete genome; segment 157/162. | Mycobacterium tuberculosis | 36,957 | 24-Jun-99 |
| | | GB_BA2:AF026540 | 1778 | AF026540 | Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds. | Mycobacterium tuberculosis | 67,627 | 30-OCT-1998 |
| | | GB_BA2:MTU96128 | 1200 | U96128 | Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds. | Mycobacterium tuberculosis | 70,417 | 25-MAR-1998 |
| rx02611 | 1775 | GB_BA1:MTCY130 | 32514 | Z73902 | Mycobacterium tuberculosis H37Rv complete genome; segment 59/162. | Mycobacterium tuberculosis | 38,532 | 17-Jun-98 |
| | | GB_BA1:MSGY151 | 37036 | AD000018 | Mycobacterium tuberculosis sequence from clone y151. | Mycobacterium tuberculosis | 60,575 | 10-DEC-1996 |
| | | GB_BA1:U00014 | 36470 | U00014 | Mycobacterium leprae cosmid B1549. | Mycobacterium leprae | 57,486 | 29-Sep-94 |
| rx02612 | 2316 | GB_BA1:MTCY130 | 32514 | Z73902 | Mycobacterium tuberculosis H37Rv complete genome; segment 59/162. | Mycobacterium tuberculosis | 38,018 | 17-Jun-98 |
| | | GB_BA1:MSGY151 | 37036 | AD000018 | Mycobacterium tuberculosis sequence from clone y151. | Mycobacterium tuberculosis | 58,510 | 10-DEC-1996 |

TABLE 4: ALIGNMENT RESULTS

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|---------|------|-------------------|--------|----------|--|-----------------------------|--------|-------------|
| rx02621 | 942 | GB_BA1:STMGLGEN | 2557 | L11647 | Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds. | Streptomyces aureofaciens | 57,193 | 25-MAY-1995 |
| | | GB_BA1:CGL133719 | 1839 | AJ133719 | Corynebacterium glutamicum yjc gene, amIR gene and citE gene, partial. | Corynebacterium glutamicum | 36,858 | 12-Aug-99 |
| | | GB_IN1:CEM108 | 39973 | Z46935 | Caenorhabditis elegans cosmid M106, complete sequence. | Caenorhabditis elegans | 37,608 | 2-Sep-99 |
| | | GB_EST29:AI547662 | 377 | AI547662 | UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0. Rattus norvegicus UI 3', mRNA sequence. | Rattus norvegicus | 50,667 | 3-Jul-99 |
| rx02640 | 1650 | GB_BA1:MTV025 | 121125 | AL022121 | Mycobacterium tuberculosis H37Rv complete genome; segment 155/162. | Mycobacterium tuberculosis | 39,187 | 24-Jun-99 |
| | | GB_BA1:PAU49666 | 4495 | U49666 | Pseudomonas aeruginosa (orfX), glycerol diffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfK) gene, partial cds. | Pseudomonas aeruginosa | 59,273 | 18-MAY-1997 |
| rx02654 | 1008 | GB_BA1:AB015974 | 1641 | AB015974 | Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds. | Pseudomonas tolaasii | 58,339 | 28-Aug-99 |
| | | GB_EST6:N65787 | 512 | N65787 | 20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B777, mRNA sequence. | Arabidopsis thaliana | 39,637 | 5-Jan-98 |
| | | GB_PL2:T17H3 | 65839 | AC005916 | Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence. | Arabidopsis thaliana | 33,735 | 5-Aug-99 |
| | | GB_RO:MMU58105 | 88871 | U58105 | Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds. | Mus musculus | 35,431 | 13-Feb-97 |
| rx02666 | 891 | GB_PR3:AC004643 | 43411 | AC004643 | Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence. | Homo sapiens | 38,851 | 01-MAY-1998 |
| | | GB_PR3:AC004643 | 43411 | AC004643 | Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence. | Homo sapiens | 41,599 | 01-MAY-1998 |
| | | GB_BA2:AF049897 | 9196 | AF049897 | Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine carbonyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds. | Corynebacterium glutamicum | 40,413 | 1-Jul-98 |
| rx02675 | 1980 | GB_BA1:PDENQOURF | 10425 | L02354 | Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds's; biotin [acetyl-CoA carboxyl] ligase (bifA) gene, complete cds. | Paracoccus denitrificans | 40,735 | 20-MAY-1993 |
| | | GB_BA1:MTCY339 | 42861 | Z77163 | Mycobacterium tuberculosis H37Rv complete genome; segment 101/162. | Mycobacterium tuberculosis | 36,471 | 17-Jun-98 |
| | | GB_BA1:MXADEVRS | 2452 | L19029 | Myxococcus xanthus devR and devS genes, complete cds's. | Myxococcus xanthus | 38,477 | 27-Jan-94 |
| rx02694 | 1065 | GB_BA1:BACLDH | 1147 | M19394 | B. caldolyticus lactate dehydrogenase (LDH) gene, complete cds. | Bacillus caldolyticus | 57,371 | 26-Apr-93 |
| | | GB_BA1:BACLDHL | 1361 | M14788 | B. stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds. | Bacillus stearothermophilus | 57,277 | 26-Apr-93 |
| | | GB_PAT:A06664 | 1350 | A06664 | B. stearothermophilus lct gene. | Bacillus stearothermophilus | 57,277 | 29-Jul-93 |
| rx02729 | 844 | GB_EST15:AA494626 | 121 | AA494626 | fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence. | Danio rerio | 50,746 | 27-Jun-97 |
| | | GB_EST15:AA494626 | 121 | AA494626 | fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence. | Danio rerio | 36,364 | 27-Jun-97 |
| rx02730 | 1161 | GB_EST19:AA758660 | 233 | AA758660 | ah67d06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence. | Homo sapiens | 37,059 | 29-DEC-1998 |
| | | GB_EST15:AA494626 | 121 | AA494626 | fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ; mRNA sequence. | Danio rerio | 42,149 | 27-Jun-97 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|--|----------------------------|--------|-------------|
| rx02737 | 1665 | GB_PR4:AC006285 | 150172 | AC006285 | Homo sapiens, complete sequence. | Homo sapiens | 37,655 | 15-Nov-99 |
| | | GB_PAT:E13655 | 2260 | E13655 | gDNA encoding glucose-6-phosphate dehydrogenase. | Corynebacterium glutamicum | 99,580 | 24-Jun-98 |
| | | GB_BA1:MTCY493 | 40790 | Z95844 | Mycobacterium tuberculosis H37Rv complete genome; segment 63/162. | Mycobacterium tuberculosis | 38,363 | 19-Jun-98 |
| | | GB_BA1:SC5A7 | 40337 | AL031107 | Streptomyces coelicolor cosmid 5A7. | Streptomyces coelicolor | 39,444 | 27-Jul-98 |
| rx02738 | 1203 | GB_PAT:E13655 | 2260 | E13655 | gDNA encoding glucose-6-phosphate dehydrogenase. | Corynebacterium glutamicum | 98,226 | 24-Jun-98 |
| | | GB_BA1:SCC22 | 22115 | AL096839 | Streptomyces coelicolor cosmid C22. | Streptomyces coelicolor | 60,399 | 12-Jul-99 |
| | | GB_BA1:SC5A7 | 40337 | AL031107 | Streptomyces coelicolor cosmid 5A7. | Streptomyces coelicolor | 36,426 | 27-Jul-98 |
| rx02739 | 2223 | GB_BA1:AB023377 | 2572 | AB023377 | Corynebacterium glutamicum tkt gene for transketolase, complete cds. | Corynebacterium glutamicum | 99,640 | 20-Feb-99 |
| | | GB_BA1:MLCL536 | 36224 | Z99125 | Mycobacterium leprae cosmid L536. | Mycobacterium leprae | 61,573 | 04-DEC-1998 |
| | | GB_BA1:U00013 | 35881 | U00013 | Mycobacterium leprae cosmid B1496. | Mycobacterium leprae | 61,573 | 01-MAR-1994 |
| rx02740 | 1053 | GB_HTG2:AC006247 | 174368 | AC006247 | Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPL-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces. | Drosophila melanogaster | 37,105 | 2-Aug-99 |
| | | GB_HTG2:AC006247 | 174368 | AC006247 | Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPL-98 48.1.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces. | Drosophila melanogaster | 37,105 | 2-Aug-99 |
| | | GB_HTG3:AC007150 | 121474 | AC007150 | Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPL-98 16.P.13 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 87 unordered pieces. | Drosophila melanogaster | 38,728 | 20-Sep-99 |
| rx02741 | 1089 | GB_HTG2:AC004951 | 129429 | AC004951 | Homo sapiens clone DJ102214, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces. | Homo sapiens | 33,116 | 12-Jun-98 |
| | | GB_HTG2:AC004951 | 129429 | AC004951 | Homo sapiens clone DJ102214, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces. | Homo sapiens | 33,116 | 12-Jun-98 |
| rx02743 | 1161 | GB_IN1:AB006546 | 931 | AB006546 | Ephydatia fluviatilis mRNA for G protein a subunit 4, partial cds. | Ephydatia fluviatilis | 36,379 | 23-Jun-99 |
| | | GB_BA1:MLCL536 | 36224 | Z99125 | Mycobacterium leprae cosmid L536. | Mycobacterium leprae | 48,401 | 04-DEC-1998 |
| | | GB_BA1:U00013 | 35881 | U00013 | Mycobacterium leprae cosmid B1496. | Mycobacterium leprae | 48,401 | 01-MAR-1994 |
| | | GB_HTG2:AC007401 | 83657 | AC007401 | Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. | Homo sapiens | 37,128 | 26-Jun-99 |
| rx02797 | 1026 | GB_BA1:CGBETPGEN | 2339 | X93514 | C.glutamicum betP gene. | Corynebacterium glutamicum | 38,889 | 8-Sep-97 |
| | | GB_GSS9:AQ148714 | 405 | AQ148714 | HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence. | Homo sapiens | 34,321 | 08-OCT-1998 |
| | | GB_BA1:BFU64514 | 3837 | U64514 | Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds. | Bacillus firmus | 38,072 | 1-Feb-97 |
| rx02803 | 680 | GB_BA1:U00020 | 36947 | U00020 | Mycobacterium leprae cosmid B229. | Mycobacterium leprae | 34,462 | 01-MAR-1994 |
| | | GB_BA2:PSU85643 | 4032 | U85643 | Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MraA (mraA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds. | Pseudomonas syringae | 50,445 | 9-Apr-97 |
| rx02821 | 363 | GB_BA1:SCSG4 | 41055 | AL031317 | Streptomyces coelicolor cosmid 6G4. | Streptomyces coelicolor | 59,314 | 20-Aug-98 |
| | | GB_HTG2:AC008105 | 91421 | AC008105 | Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces. | Homo sapiens | 37,607 | 22-Jul-99 |
| | | GB_HTG2:AC008105 | 91421 | AC008105 | Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces. | Homo sapiens | 37,607 | 22-Jul-99 |
| | | GB_EST33:AV117143 | 222 | AV117143 | AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610200J17, mRNA sequence. | Mus musculus | 40,157 | 30-Jun-99 |

TABLE 4: ALIGNMENT RESULTS

| | | | | | | | | |
|---------|------|-------------------|--------|----------|---|-------------------------------|--------|-------------|
| rs02829 | 373 | GB_HTG1:HSU9G8 | 48735 | AL008714 | Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Homo sapiens | 41,595 | 23-Nov-99 |
| | | GB_HTG1:HSU9G8 | 48735 | AL008714 | Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces. | Homo sapiens | 41,595 | 23-Nov-99 |
| | | GB_PR3:HSUJ85B5 | 39550 | Z69724 | Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X. | Homo sapiens | 41,595 | 23-Nov-99 |
| rs03216 | 1141 | GB_HTG3:AC008184 | 151720 | AC008184 | Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces. | Drosophila melanogaster | 39,600 | 2-Aug-99 |
| | | GB_EST15:AA477537 | 411 | AA477537 | zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element; contains element HGR repetitive element ;, mRNA sequence. | Homo sapiens | 37,260 | 9-Nov-97 |
| | | GB_EST26:AI330662 | 412 | AI330662 | fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5' mRNA sequence. | Danio rerio | 37,805 | 28-DEC-1998 |
| rs03215 | 1038 | GB_BA1:SC3F9 | 19830 | AL023862 | Streptomyces coelicolor cosmid 3F9. | Streptomyces coelicolor A3(2) | 48,657 | 10-Feb-99 |
| | | GB_BA1:SLINC | 36270 | X79146 | S.lincolnensis (78-11) Lincomycin production genes. | Streptomyces lincolnensis | 39,430 | 15-MAY-1996 |
| | | GB_HTG5:AC009660 | 204320 | AC009660 | Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces. | Homo sapiens | 35,151 | 04-DEC-1999 |
| rs03224 | 1288 | GB_PR3:AC004076 | 41322 | AC004076 | Homo sapiens chromosome 19, cosmid R30217, complete sequence. | Homo sapiens | 37,788 | 29-Jan-98 |
| | | GB_PL2:SPAC926 | 23193 | AL110469 | S.pombe chromosome I cosmid c926. | Schizosaccharomyces pombe | 38,474 | 2-Sep-99 |
| | | GB_BA2:AE001081 | 11473 | AE001081 | Archaeoglobus fulgidus section 26 of 172 of the complete genome. | Archaeoglobus fulgidus | 35,871 | 15-DEC-1997 |